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(57) Abstract

Novel anti-Factor IX Fab fragment crystalline structures are identified. Methods of identifying peptidomimetics of these fragments are disclosed.

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CRYSTAL STRUCTURES OF ANTI-FACTOR IX Fab FRAGMENTS AND METHODS OF USE FOR PEPTIDOMIMETIC DESIGN

This application claims the benefit of U.S. Provisional Application No. 60/051,645, filed 3 July 1997.

FIELD OF THE INVENTION

This invention relates to anti-Factor IX Fab fragment crystals and the use of complementarity determining region (CDR) structural parameters for design and selection of peptidomimetics.

BACKGROUND OF THE INVENTION

Under normal circumstances, an injury, be it minor or major, to vascular endothelial cells lining a blood vessel triggers a hemostatic response through a sequence of events commonly r. .rred to as the coagulation "cascade." The cascade culminates in the conversion of soluble fibrinogen to insoluble fibrin which, together with platelets, forms a localized clot or thrombus which prevents extravasation of blood components. Wound healing can then occur followed by clot dissolution and restoration of blood vessel integrity and flow.

The events which occur between injury and clot formation are a carefully regulated and linked series of reactions. In brief, a number of plasma coagulation proteins in inactive proenzyme forms and cofactors circulate in the blood. Active enzyme complexes are assembled at an injury site and are sequentially activated to serine proteases, with each successive serine protease catalyzing the subsequent proenzyme to protease activation. This enzymatic cascade results in each step magnifying the effect of the succeeding step. For an overview of the coagulation cascade see the first chapter of "Thombosis and Hemorrhage", J. Loscalzo and A. Schafer, eds., Blackwell Scientific Publications, Oxford, England (1994).

While efficient clotting limits the loss of blood at an injury site, inappropriate formation of thrombi in veins or arteries is a common cause of disability and death. Abnormal clotting activity can result in and/or from pathologies or treatments such as myocardial infarction, unstable angina, atrial fibrillation, stroke, renal damage, percutaneous translumenal coronary angioplasty, disseminated intravascular coagulation, sepsis, pulmonary embolism and deep vein thrombosis. The formation of clots on foreign

surfaces of artificial organs, shunts and prostheses such as artificial heart valves is also problematic.

Approved anticoagulant agents currently used in treatment of these pathologies and other thrombotic and embolic disorders include the sulfated heteropolysaccharides heparin and low molecular weight (LMW) heparin. These agents are administered parenterally and can cause rapid and complete inhibition of clotting by activation of the thrombin inhibitor, antithrombin III and inactivation of all of the clotting factors.

However, due to their potency, heparin and LMW heparin suffer drawbacks. Uncontrolled bleeding as a result of the simple stresses of motion and accompanying contacts with physical objects or at surgical sites is the major complication and is observed in 1 to 7% of patients receiving continuous infusion and in 8 to 14% of patients given intermittent bolus doses. To minimize this risk, samples are continuously drawn to enable *ex vivo* clotting times to be continuously monitored, which contributes substantially to the cost of therapy and the patient's inconvenience.

Further, the therapeutic target range to achieve the desired level of efficacy without placing the patient at risk for bleeding is narrow. The therapeutic range is approximately 1 to less than 3 ug heparin/ml plasma which results in activated partial thromboplastin time (aPTT) assay times of about 35 to about 100 seconds. Increasing the heparin concentration to 3 ug/ml exceeds the target range and at concentrations greater than 4 ug/ml, clotting activity is not detectable. Thus, great care must be taken to keep the patient's plasma concentrations within the therapeutic range.

Another approved anticoagulant with slower and longer lasting effect is warfarin, a coumarin derivative. Warfarin acts by competing with Vitamin K dependent post-translational modification of prothrombin and other Vitamin K-dependent clotting factors.

The general pattern of anticoagulant action,in which blood is rendered non-clottable at concentrations only slightly higher than the therapeutic range is seen for warfarin as well as for heparin and LMW heparin. Clearly, a need exists for an anticoagulant agent which is efficacious in controlling thrombotic and embolic disorders yet does not cause uncontrolled bleeding or its possibility. Accordingly, there is also a need for anticoagulant agent structural information to enable identification and structure-based design of new anticoagulant agents.

SUMMARY OF THE INVENTION

Accordingly, an aspect of the present invention is a BC2 Fab fragment crystal.

Another aspect of the invention is a Fab fragment crystal containing BC2 CDRs.

Another aspect of the invention is a SB249417 Fab fragment crystal.

Another aspect of the invention is a method for identifying a peptidomimetics having Factor IX binding activity comprising the steps of searching a small molecule structural database with CDR structural parameters derived from anti-Factor IX Fab fragment crystals; selecting a molecular structure from the database which mimics the CDR structural parameters; synthesizing the selected molecular structure; and screening the synthesized molecule for Factor IX binding activity.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a three-dimensional structure of the residues of BC2 HC-CDR1.

Figure 2 is a three-dimensional structure of the residues of BC2 HC-CDR2.

Figure 3 is a three-dimensional structure of the residues of BC2 HC-CDR3.

Figure 4 is a three-dimensional structure of the residues of BC2 LC-CDR1.

Figure 5 is a three-dimensional structure of the residues of BC2 LC-CDR2.

Figure 6 is a three-dimensional structure of the residues of BC2 LC-CDR3.

Figure 7 is a three-dimensional structure of the residues of SB249417 HC-CDR1.

Figure 8 is a three-dimensional structure of the residues of SB249417 HC-CDR2.

Figure 9 is a three-dimensional structure of the residues of SB249417 HC-CDR3.

Figure 10 is a three-dimensional structure of the residues of SB249417 LC-CDR1.

Figure 11 is a three-dimensional structure of the residues of SB249417 LC-CDR2.

Figure 12 is a three-dimensional structure of the residues of SB249417 LC-CDR3.

DETAILED DESCRIPTION OF THE INVENTION

All publications, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference as though fully set forth.

Factor IX (fIX) is a vitamin K-dependent serine protease zymogen which plays an important role in the amplification of the blood coagulation cascade by catalyzing the activation of factor X on the membrane surface in the presence of activated factor VIII and calcium. Murine anti-human factor IX monoclonal antibody (mAb) BC2, as described in U.S. Patent Application No. 08/783,853 is an IgG1 kappa monoclonal antibody having

useful properties for anticoagulant therapy in arterial and venous thrombosis. BC2 down-regulates the blood clotting cascade in a self-limiting manner. BC2 inhibits the activation of fIX to fIXa by fXI as well as its activation by the complex of tissue factor and fVIIa. BC2 also inhibits fIXa coagulant activity. BC2 binds to human fIX and fIXa in a calcium-dependent manner with a dissociation constant Kd=4 nM. BC2 also cross-reacts with and inhibits rat fIX.

Humanized constructs of BC2 have been made and tested for anticoagulant activity *in vitro* and in animal models. These constructs are described in U.S. Patent Application No. 08/783,853 and, like BC2, are novel anticoagulants exhibiting self-limiting, neutralizing activity, namely they down-regulate the blood clotting cascade in a self-limiting manner, minimizing the bleeding risks associated with heparin and other anticoagulant therapies. One such humanized construct of BC2 is SB249417. As used herein, the term "self-limiting, neutralizing activity" refers to the activity of a peptidomimetic that binds to human coagulation factor IX or IXa and inhibits thrombosis in a manner such that limited modulation of coagulation is produced. "Limited modulation of coagulation" is defined as an increase in clotting time, as measured by prolongation of the activated partial thromboplastin time (aPTT), where plasma remains clottable with aPTT reaching a maximal value despite increasing concentrations of monoclonal antibody. This limited modulation of coagulation is in contrast to plasma being rendered unclottable and exhibiting an infinite aPTT in the presence of increasing concentrations of heparin. Preferably, the maximal aPTT values are within the heparin therapeutic range. Most preferably, maximal aPTT is within the range of about 35 seconds to about 100 seconds which corresponds to about 1.5 times to about 3.5 times the normal control aPTT value.

In the humanization process, the mouse antibody framework is changed to that from a human antibody, leaving the antigen-binding site unchanged. This site is formed by certain regions in the mAb amino acid sequence which are termed the complementarity determining regions (CDRs), or hypervariable segments. The antigen-binding site, which determines its specificity to its antigen, is located in the Fab fragment of the antibody, which consists of the entire light chain (LC) and part of the heavy chain (HC).

As part of an effort to develop functional small-molecule mimics of these therapeutic macromolecules, the structural and mechanistic features of the anticoagulant activity of the anti-fIX mAbs BC2 and SB249417 have been determined. This information is useful for design and testing of small peptides that functionally mimic the mAb's anticoagulant properties and to develop these peptides for therapeutic use.

The three-dimensional structures of the Fab fragments of BC2 and SB249417 were determined using X-ray crystallography as described in the Examples. The structural information can be stored on a computer-readable medium.

The CDRs from the mouse and humanized Fab fragments have generally similar conformations. R.m.s. differences between corresponding CDR C_α positions between the two Fabs are below 0.5 Å, except in HC-CDR2 and HC-CDR3 where r.m.s. values are 1.97 and 3.7 Å, respectively. The slight change in the conformations of HC-CDR2 and HC-CDR3 amount to an angular shift in the planes of these loops, keeping the angle between them unchanged. In both Fabs, the three HC CDRs and LC-CDR3 form a groove (27 Å long, 8 Å wide and 9 Å deep) which runs through the CDR surface. CDR residues HC-Asn35, HC-Trp50, and LC-Arg95, which line a deep hole in the center of the groove, are considered important for antigen binding.

Structural information obtained for the CDRs of the BC2 and SB249417 Fab structures is useful for discovery of small molecule peptidomimetics. Preferred peptidomimetics include peptides and synthetic organic molecules which bind to Factor IX and have self-limiting, neutralizing activity in an in vitro clotting assay. An exemplary approach to such a structure-based peptide mimic design follows (Zhao, *et al.*, 1995; Monfardini C. *et al.*, 1996).

A search of several small-molecule structural data bases such as Available Chemicals Directory, Cambridge Crystallographic Database, Fine Chemical Database and CONCORD database (for a review, see Rusinko A., 1993) is carried out using parameters derived from the CDR structures. The search can be 2-dimensional, 3-dimensional or both and can be done using a combination of software such as UNITY version 2.3.1 (Tripos, Inc.), MACCS 3D, CAVEAT and DOCK. Conformational flexibility of the small molecules is allowed. The strategy for conducting the search takes into account conformations of individual CDRs as well as combinations of CDRs and/or key residues in the mAb combining site.

An initial approach is to focus on structural parameters from HC-CDR3, LC-CDR3 and HC-CDR2 since these CDRs have been found in other Fabs to participate intimately in antigen recognition. A search for small-molecule mimics of HC-CDR3, LC-CDR3 and HC-CDR2 is separately conducted. The structural parameters from each two of these three CDRs are combined and the search repeated. The next step will be using parameters from all three CDRs. The conformational parameters of the remaining three CDRs will be included at a later stage, resulting in a search combining all six CDRs. Pref rably, the

selected molecular structure mimics the parameters of CDR residues HC-Asn35, HC-Trp50, and LC-Arg95. Small-molecule hits resulting from the searches are synthesized and screened for factor-IX binding in an ELISA assay and preferably, for anti-thrombotic activity in a standard *in vitro* clotting assay. Most preferably, the hits will also exhibit self-limiting, neutralizing activity.

Peptidomimetics produced by the method of the invention are expected to be useful in therapy of thrombotic and embolic disorders such as those associated with myocardial infarction, unstable angina, atrial fibrillation, stroke, renal damage, pulmonary embolism, deep vein thrombosis, percutaneous translumenal coronary angioplasty, disseminated intravascular coagulation, sepsis, artificial organs, shunts or prostheses.

The present invention will now be described with reference to the following specific, non-limiting examples.

Example 1
Preparation and Purification of Fab Fragments

Both BC2 and SB249417 Fab fragments were prepared and purified as follows. 50 mL of freshly purified monoclonal anti-human fIX antibody sample (1.2mg/mL in PBS buffer) was concentrated in an Amicon cell using a 30-kDa molecular weight cutoff membrane (YM30, at 65 psi, 4°C) to a final volume of 5.0 mL and final concentration of 12.0 mg/mL. A papain digest of the mAb was started by adding to the concentrated mAb sample 20μg/mL papain (Boehringer Manheim, cat.# 108014), 2.5 mM EDTA (pH 7.5) and 5.0 mM cysteine-HCL monohydrate (PIERCE, cat.# 44889) and incubating the mixture at 37°C for 4 hours and shaking gently. The reaction was stopped by cooling the mixture on ice for 20 min.

The Fc fragment was removed by incubating the digest with 5 mL of protein A-Sepharose resin (Pharmacia) and mixing at 4°C for 1 hour. The mixture was transferred into a 15 mL gravity-fed column, and the unbound fraction (containing the Fab fragment) was collected. The column was washed twice with a 8 mL volume of 20mM Na_2HPO_4, 150mM NaCl, pH 7.5. The eluate and 2 washes were pooled and concentrated to 5.3 mL using an Amicon cell with a YM10 membrane at 4°C.

The sample was loaded on a Pharmacia Superdex 75 column (volume 320mL), pre-equilibrated with 20mM Na_2HPO_4, 150mM NaCl, pH 7.5. The column was then eluted with the same buffer at a rate of 2.5 mL/min, and 1 mL fractions collected after 30 min of void-volume collection. The Fab fragment eluted as a single molecular species as indicated

by a large A_{280} peak appearing in fractions 26-36, which were pooled and assayed for protein concentration by A_{280} absorption. A total of 25 mg of Fab were generated using this standard protocol (purification yield = 50-60%). SDS-PAGE analysis of the Superdex 75 eluate revealed a single species with an apparent molecular weight of 47,000Da.

IEF analysis of the BC2 Fab sample revealed the presence of multiple isoelectric variants; the two major isoforms have apparent pI values of 8.9 and 7.35. These two species were separated using an ion exchange chromatography step which proved necessary and sufficient for obtaining usable crystals. The 25 mg SEC eluate was buffer exchanged by thorough and repeated dialysis against 20mM Tris, pH 9.2, concentrated to 5 mL in an Amicon cell, and loaded on a 1 mL Pharmacia Mono Q column, pre-equilibrated with buffer A (20mM Tris, pH 9.2). The column was washed with 10 mL buffer A, and no protein eluted in the flow through. Three protein species were eluted with a 0-15% gradient of buffer B (20mM Tris, pH 9.2, 1.0M NaCl) followed by a 15-100% gradient of buffer B, at a rate of 1.0mL/min. 1 mL fractions were collected. Fractions corresponding to the first (sharp) peak in the chromatogram were pooled, assayed for A_{280} absorption, buffer exchanged in an Amicon cell against 20mM HEPES, pH 7.4, concentrated to 8mg/mL and used for crystallization. Fractions from the other two peaks did not crystallize. The final yield of the protocol was approximately 36% (crystallizable fraction only).

Example 2

Crystallization of Fab Fragments

BC2 Fab: Protein isoform from peak 1 of the ion exchange step was crystallized using the vapor diffusion method in a sitting-drop setup. The well solution contained 14% PEG6K, 20mM ammonium sulfate (or 100mM LiCl), 10mM $CaAc_2$ and 200mM imidazole/HEPES, pH 7.0. The drops were prepared by mixing 3 µL of the well solution with 3 µL of protein solution (8mg/mL in 20mM HEPES, pH 7.0). Large orthorhombic crystals grew in 5 days at 21 °C to a size of 0.8x0.3x0.25 mm^3. The crystals diffracted to 3.0 Å, in space group P21212, unit cell dimensions a=89.3, b=120.6, c=43.4 Å, and one molecule in the asymmetric unit.

SB249417 Fab: A similar sitting drop method was used. The well solution contained 30-40% saturated ammonium sulfate and 50mM MES, pH 6.0. The drops were prepared by mixing equal volumes of well solution and protein solution (10 mg/mL in 10 mM HEPES, pH 7.0). Large crystals grew in one week at 15 °C to a size of 0.6x0.4x0.3

mm^3. The crystals diffracted to 2.2 Å, in space group P1, unit cell dimensions a=56.6, b=56.6, c=73.7 Å, α=86.0, β= 86.0, γ= 64.9°, and two molecules in the asymmetric unit.

Example 3

X-Ray Data Collection

X-ray diffraction data were collected on a MAR area detector mounted on a Rigaku high-brilliance source operated at 50 kV/100 mA with monochromatic CuK_α radiation in 1° oscillations frames. Data from three and two different crystals were collected, merged and used for structure determination of the BC2 Fab and SB249417 Fab, respectively. All data were processed using the HKL program, edition 4 (Otwinowski, 1993). Table 1 summarizes the data collection parameters.

For BC2, the merged data were used for structure determination, whereas structure refinement was done against a single-crystal data set with the best R-sym values. For SB249417, merged data were used for structure determination and refinement.

Table 1: Summary of X-ray Diffraction Data.

Parameter	BC2	249417
cell a,b,c (Å) alpha, beta, gamma	89.60, 120.69, 43.58 90.0, 90.0, 90.0 deg.	56.6, 56.6, 73.7 86.0, 86.0, 64.9 deg.
Resolution (Å)	3.0	2.2
Number of observed reflections	132,951	145,877
Number of unique reflections	12,211	21,122
mosaicity	0.16	0.22
$\langle I/\sigma \rangle$	11.5	7.0
Completeness	99.7	99.9
% of data >2 σ	76.0	71.4
R-sym	0.12	0.07

Example 4

Structure Determinati n

The structures of the Fabs were determined using generalized molecular replacement methods following the standard protocol of Brünger (1991). The procedure includes a real-space cross-rotation Patterson search (Huber, 1985) followed by Patterson coefficient (PC) refinement (Brünger, 1990), a translation search, and finally rigid-body refinement. The X-PLOR program suite was used (Brünger, 1992) for all four steps.

A search model was constructed for BC2 from the PDB-deposited 1.9Å structures of two Fabs: the light chain model from murine IgG2a Fab that neutralizes human rhinovirus 14 (PDB entry 1FOR), and the heavy chain model from murine idiotype Fab 730.1.4 (PDB entry 1IAI). The two were combined by least-square fitting of the two-chain models. Sequence identity of the resulting probe with BC2 Fab is as follows:

V_L 84%

C_L 100%

V_H 84%

C_H1 95%,

A similar search model was constructed for SB249417 from the PDB-deposited 3.0 Å humanized anti-CD18 antibody Fab fragment (PDB entry 2FGW). Sequence identity of the search model with SB249417 Fab is as follows:

V_L	81%
C_L	100%
V_H	59%
C_H1	99%

In eachmodel, residues different from those in the amino acid sequence of the Fab were mutated to alanine.

In the case of BC2, a cross-rotation search was done with this model which represents the entire asymmetric unit. Eulerian space was searched in the rotation-function's asymmetric unit ($0 \le \theta_1 < 2\pi$, $0 \le \theta_2 \le \pi/2$, $0 \le \theta_3 < \pi$, where θ_1, θ_2, θ_3 are the Eulerian angles as defined by Rossmann & Blow (1962)) with a constant increment of 2.5° in each dimension. Data in the resolution range 15.0-4.0 Å was used in this search. The top 6000 peaks of the rotation function (RF) were used for cluster analysis. The solutions of the rotation function were then subjected to PC refinement followed by rigid-body minimization of the solution with the highest PC value. The latter was done in three steps: 1) treating the entire molecular model as a rigid body, 2) treating the heavy chain and light

chain each as a rigid body and 3) treating the variable (V_H and V_L) and constant (C_H1 and C_L) domains of each chain as a rigid body.

In the case of SB249417, an initial self-rotation search converged to a single solution representing a non-crystallographic two-fold axis defined by spherical angles psi, phi = 147, 0. A cross-rotation search ($0 \leq \theta_1 < 2\pi$, $0 \leq \theta_2 \leq \pi$, $0 \leq \theta_3 < 2\pi$) was followed by PC refinement, resulting in two solutions, which were related by non-crystallographic symmetry.

Using the structure corresponding to the highest RF peak after PC refinement (one peak in the case of BC2 and two peaks related by NCS in the case of SB249417) and 15.0-4.0Å data, a translation search was carried out. For BC2, the search was restricted to half of the unit cell in all three dimensions. For SB249417, NCS was directly applied to the translation function solution to generate the other molecule in the P1 cell. For each Fab, the structure corresponding to the top solution of the translation function was then rigid-body refined as described above.

The rigid-body refined structure was then used to phase the reflections from a single-crystal data set, in the case of BC2, or merged data from multiple crystals in the case of SB249417. F_o-F_c and $2F_o$-F_c electron density maps were calculated and inspected. The model was re-built to fit the map in the CDR regions and elsewhere using the true amino acid sequence of the Fab. The structures were refined using the simulated annealing protocols of X-PLOR (Brünger, 1992). Refinement parameters are summarized in Table 2.

Table 2:Structure Refinement Statistics

Parameter	BC2	SB249417
Space group	$P2_1\,2_1\,2$	P1
Observations (N)	47,643	145,877
Unique reflections (N)	11,353	40,746
R-sym (on I, %)	0.09	0.07
Average I/s	8.8	7.1
Reflections use in refinement (N)	8469	36,628
Completeness of refinement data	92.2	94.3
Refinement resolution range (Å)	20.0-3.0	15.0-2.2
Atoms used in refinement (N)	3157	6481
R_{cryst} (%)	22.0	23.0
R_{free} (%)	29.0	27.9
R.m.s. deviations from standard values:		
Bond length (Å)	0.019	0.014
Bond angles (deg.)	3.3	1.27
Mean B-factor ($Å^2$)	29.0	27.3

Like all Fab fragments, BC2 and SB249417 Fab structures are made up of a tetrahedral array of four globular domains – V_L, V_H, C_L and C_H1 – which follow the immunoglobulin fold. Each domain is constituted of two broad sheets of antiparallel β-strands held together by hydrophobic interactions. The CDR loops are ordered with varying temperature-factor values. The three-dimensional coordinates of the residues belonging to all six CDRs of BC2 and SB249417 are listed in Tables 3-8 and Tables 9-14, respectively. Figures 1-6 and 7-12 show the corresponding three dimensional structures.

Table 3: Three dimensi nal coordinates of HC - CDR1 (HC: ASN31 - ASN35) from BC2

					x	y	z	Q	B
ATOM	2287	N	ASN	31	38.145	52.427	-13.427	1.00	48.47
ATOM	2289	CA	ASN	31	37.357	53.503	-12.856	1.00	48.47
ATOM	2290	CB	ASN	31	35.961	53.611	-13.477	1.00	49.47
ATOM	2291	CG	ASN	31	35.742	52.671	-14.676	1.00	49.47
ATOM	2292	OD1	ASN	31	36.684	52.260	-15.365	1.00	49.47
ATOM	2293	ND2	ASN	31	34.477	52.330	-14.916	1.00	49.47
ATOM	2296	C	ASN	31	37.231	53.540	-11.325	1.00	48.47
ATOM	2297	O	ASN	31	36.898	54.595	-10.776	1.00	49.47
ATOM	2298	N	TYR	32	37.491	52.428	-10.636	1.00	55.29
ATOM	2300	CA	TYR	32	37.341	52.392	-9.167	1.00	55.29
ATOM	2301	CB	TYR	32	36.051	51.709	-8.737	1.00	25.46
ATOM	2302	CG	TYR	32	34.839	51.959	-9.549	1.00	25.46
ATOM	2303	CD1	TYR	32	34.842	51.790	-10.936	1.00	25.46
ATOM	2304	CE1	TYR	32	33.672	51.848	-11.656	1.00	25.46
ATOM	2305	CD2	TYR	32	33.642	52.198	-8.911	1.00	25.46
ATOM	2306	CE2	TYR	32	32.466	52.244	-9.600	1.00	25.46
ATOM	2307	CZ	TYR	32	32.475	52.071	-10.966	1.00	25.46
ATOM	2308	OH	TYR	32	31.269	52.059	-11.601	1.00	25.46
ATOM	2310	C	TYR	32	38.442	51.679	-8.402	1.00	55.29
ATOM	2311	O	TYR	32	38.845	50.570	-8.772	1.00	25.46
ATOM	2312	N	GLY	33	38.774	52.229	-7.237	1.00	17.19
ATOM	2314	CA	GLY	33	39.817	51.656	-6.405	1.00	17.19
ATOM	2315	C	GLY	33	39.406	50.378	-5.697	1.00	17.19
ATOM	2316	O	GLY	33	38.237	50.200	-5.296	1.00	65.52
ATOM	2317	N	MET	34	40.382	49.487	-5.526	1.00	36.25
ATOM	2319	CA	MET	34	40.143	48.215	-4.854	1.00	36.25
ATOM	2320	CB	MET	34	40.888	47.087	-5.555	1.00	15.05
ATOM	2321	CG	MET	34	40.667	45.723	-4.926	1.00	15.05
ATOM	2322	SD	MET	34	38.944	45.396	-4.815	1.00	15.05
ATOM	2323	CE	MET	34	38.703	44.674	-6.413	1.00	15.05
ATOM	2324	C	MET	34	40.635	48.287	-3.430	1.00	36.25
ATOM	2325	O	MET	34	41.514	49.072	-3.107	1.00	15.05
ATOM	2326	N	ASN	35	40.072	47.454	-2.570	1.00	16.44
ATOM	2328	CA	ASN	35	40.513	47.391	-1.182	1.00	16.44
ATOM	2329	CB	ASN	35	39.359	47.668	-0.196	1.00	23.13
ATOM	2330	CG	ASN	35	38.947	49.118	-0.149	1.00	23.13
ATOM	2331	OD1	ASN	35	38.491	49.623	0.888	1.00	23.13
ATOM	2332	ND2	ASN	35	39.065	49.793	-1.275	1.00	23.13
ATOM	2335	C	ASN	35	41.038	45.954	-0.980	1.00	16.44
ATOM	2336	O	ASN	35	41.058	45.182	-1.920	1.00	23.13

Table 4: Three dimensional coordinates of HC - CDR2 (HC: TRP50 - GLY66) from BC2

					x	y	z	Q	B
ATOM	2474	N	TRP	50	45.028	49.852	-0.044	1.00	2.00
ATOM	2476	CA	TRP	50	44.159	50.501	-1.002	1.00	2.00
ATOM	2477	CB	TRP	50	44.044	51.944	-0.556	1.00	57.49
ATOM	2478	CG	TRP	50	42.874	52.695	-1.042	1.00	57.49
ATOM	2479	CD2	TRP	50	42.803	53.588	-2.163	1.00	57.49
ATOM	2480	CE2	TRP	50	41.556	54.226	-2.120	1.00	57.49
ATOM	2481	CE3	TRP	50	43.669	53.919	-3.196	1.00	57.49
ATOM	2482	CD1	TRP	50	41.703	52.803	-0.412	1.00	57.49
ATOM	2483	NE1	TRP	50	40.904	53.723	-1.037	1.00	57.49
ATOM	2485	CZ2	TRP	50	41.155	55.182	-3.058	1.00	57.49
ATOM	2486	CZ3	TRP	50	43.267	54.872	-4.132	1.00	57.49
ATOM	2487	CH2	TRP	50	42.033	55.486	-4.056	1.00	57.49
ATOM	2488	C	TRP	50	44.923	50.556	-2.296	1.00	2.00
ATOM	2489	O	TRP	50	46.141	50.436	-2.292	1.00	57.49
ATOM	2490	N	ILE	51	44.239	50.756	-3.407	1.00	2.58
ATOM	2492	CA	ILE	51	44.957	50.921	-4.652	1.00	2.58
ATOM	2493	CB	ILE	51	45.528	49.623	-5.217	1.00	4.23
ATOM	2494	CG2	ILE	51	44.516	48.983	-6.161	1.00	4.23
ATOM	2495	CG1	ILE	51	46.800	49.968	-5.991	1.00	4.23
ATOM	2496	CD1	ILE	51	47.581	48.788	-6.481	1.00	4.23
ATOM	2497	C	ILE	51	44.113	51.616	-5.693	1.00	2.58
ATOM	2498	O	ILE	51	42.925	51.332	-5.854	1.00	4.23
ATOM	2499	N	ASN	52	44.738	52.546	-6.398	1.00	33.49
ATOM	2501	CA	ASN	52	44.042	53.268	-7.441	1.00	33.49
ATOM	2502	CB	ASN	52	44.451	54.725	-7.525	1.00	15.27
ATOM	2503	CG	ASN	52	43.618	55.455	-8.514	1.00	15.27
ATOM	2504	OD1	ASN	52	43.668	55.173	-9.715	1.00	15.27
ATOM	2505	ND2	ASN	52	42.740	56.301	-8.015	1.00	15.27
ATOM	2508	C	ASN	52	44.369	52.571	-8.732	1.00	33.49
ATOM	2509	O	ASN	52	45.373	52.841	-9.404	1.00	15.27
ATOM	2510	N	THR	53	43.386	51.808	-9.129	1.00	16.45
ATOM	2512	CA	THR	53	43.414	50.928	-10.257	1.00	16.45
ATOM	2513	CB	THR	53	42.142	50.216	-10.205	1.00	42.20
ATOM	2514	OG1	THR	53	41.089	51.138	-10.536	1.00	42.20
ATOM	2516	CG2	THR	53	41.936	49.718	-8.773	1.00	42.20
ATOM	2517	C	THR	53	43.536	51.480	-11.656	1.00	16.45
ATOM	2518	O	THR	53	42.981	50.923	-12.616	1.00	42.20
ATOM	2519	N	ARG	54	44.229	52.583	-11.795	1.00	50.54
ATOM	2521	CA	ARG	54	44.366	53.184	-13.107	1.00	50.54
ATOM	2522	CB	ARG	54	43.377	54.373	-13.131	1.00	42.70
ATOM	2523	CG	ARG	54	43.078	54.966	-14.495	1.00	42.70
ATOM	2524	CD	ARG	54	43.317	56.486	-14.569	1.00	42.70
ATOM	2525	NE	ARG	54	42.980	56.929	-15.921	1.00	42.70
ATOM	2527	CZ	ARG	54	43.854	57.134	-16.902	1.00	42.70
ATOM	2528	NH1	ARG	54	45.163	56.985	-16.697	1.00	42.70
ATOM	2531	NH2	ARG	54	43.407	57.341	-18.139	1.00	42.70
ATOM	2534	C	ARG	54	45.798	53.722	-13.122	1.00	50.54
ATOM	2535	O	ARG	54	46.453	53.897	-14.161	1.00	42.70
ATOM	2536	N	ASN	55	46.349	53.636	-11.933	1.00	22.51
ATOM	2538	CA	ASN	55	47.588	54.260	-11.622	1.00	22.51
ATOM	2539	CB	ASN	55	47.182	55.219	-10.536	1.00	62.29
ATOM	2540	CG	ASN	55	48.043	56.422	-10.448	1.00	62.29
ATOM	2541	OD1	ASN	55	48.996	56.618	-11.205	1.00	62.29
ATOM	2542	ND2	ASN	55	47.679	57.279	-9.517	1.00	62.29
ATOM	2545	C	ASN	55	48.594	53.325	-11.040	1.00	22.51
ATOM	2546	O	ASN	55	49.771	53.374	-11.369	1.00	62.29
ATOM	2547	N	GLY	56	48.129	52.529	-10.088	1.00	49.54
ATOM	2549	CA	GLY	56	49.031	51.639	-9.397	1.00	49.54
ATOM	2550	C	GLY	56	49.476	52.347	-8.124	1.00	49.54
ATOM	2551	O	GLY	56	50.042	51.719	-7.214	1.00	47.80
ATOM	2552	N	LYS	57	49.244	53.661	-8.044	1.00	54.37
ATOM	2554	CA	LYS	57	49.608	54.400	-6.833	1.00	54.37
ATOM	2555	CB	LYS	57	49.354	55.911	-6.963	1.00	38.06
ATOM	2556	CG	LYS	57	50.526	56.635	-7.654	1.00	38.06
ATOM	2557	CD	LYS	57	50.180	58.024	-8.266	1.00	38.06
ATOM	2558	CE	LYS	57	50.217	59.176	-7.281	1.00	38.06
ATOM	2559	NZ	LYS	57	51.151	60.258	-7.772	1.00	38.06
ATOM	2563	C	LYS	57	48.819	53.662	-5.761	1.00	54.37
ATOM	2564	O	LYS	57	47.726	53.131	-6.030	1.00	38.06
ATOM	2565	N	SER	58	49.419	53.582	-4.581	1.00	54.98
ATOM	2567	CA	SER	58	48.887	52.742	-3.525	1.00	54.98
ATOM	2568	CB	SER	58	49.664	51.452	-3.702	1.00	58.93
ATOM	2569	OG	SER	58	51.012	51.786	-4.083	1.00	58.93
ATOM	2571	C	SER	58	49.025	53.181	-2.050	1.00	54.98
ATOM	2572	O	SER	58	50.106	53.608	-1.630	1.00	58.93
ATOM	2573	N	THR	59	47.982	52.953	-1.247	1.00	34.76
ATOM	2575	CA	THR	59	47.991	53.360	0.163	1.00	34.76
ATOM	2576	CB	THR	59	46.808	54.265	0.424	1.00	50.04

Cont./ Table 4

					x	y	z	Q	B
ATOM	2577	OG1	THR	59	46.669	55.185	-0.672	1.00	50.04
ATOM	2579	CG2	THR	59	47.012	55.055	1.720	1.00	50.04
ATOM	2580	C	THR	59	47.812	52.183	1.085	1.00	34.76
ATOM	2581	O	THR	59	46.880	51.425	0.888	1.00	50.04
ATOM	2582	N	TYR	60	48.648	52.037	2.111	1.00	21.76
ATOM	2584	CA	TYR	60	48.543	50.877	3.040	1.00	21.76
ATOM	2585	CB	TYR	60	49.768	49.964	2.990	1.00	21.25
ATOM	2586	CG	TYR	60	50.373	49.642	1.661	1.00	21.25
ATOM	2587	CD1	TYR	60	49.743	49.934	0.468	1.00	21.25
ATOM	2588	CE1	TYR	60	50.336	49.623	-0.751	1.00	21.25
ATOM	2589	CD2	TYR	60	51.614	49.022	1.600	1.00	21.25
ATOM	2590	CE2	TYR	60	52.191	48.699	0.407	1.00	21.25
ATOM	2591	CZ	TYR	60	51.557	49.000	-0.763	1.00	21.25
ATOM	2592	OH	TYR	60	52.147	48.629	-1.923	1.00	21.25
ATOM	2594	C	TYR	60	48.452	51.284	4.495	1.00	21.76
ATOM	2595	O	TYR	60	49.056	52.274	4.882	1.00	21.25
ATOM	2596	N	VAL	61	47.793	50.459	5.307	1.00	2.00
ATOM	2598	CA	VAL	61	47.636	50.717	6.748	1.00	2.00
ATOM	2599	CB	VAL	61	46.724	49.642	7.436	1.00	36.32
ATOM	2600	CG1	VAL	61	47.388	49.056	8.727	1.00	36.32
ATOM	2601	CG2	VAL	61	45.318	50.258	7.783	1.00	36.32
ATOM	2602	C	VAL	61	48.997	50.684	7.395	1.00	2.00
ATOM	2603	O	VAL	61	49.909	50.132	6.812	1.00	36.32
ATOM	2604	N	ASP	62	49.126	51.225	8.610	1.00	69.13
ATOM	2606	CA	ASP	62	50.439	51.226	9.291	1.00	69.13
ATOM	2607	CB	ASP	62	50.443	52.071	10.580	1.00	34.42
ATOM	2608	CG	ASP	62	50.989	53.499	10.376	1.00	34.42
ATOM	2609	OD1	ASP	62	51.241	54.198	11.375	1.00	34.42
ATOM	2610	OD2	ASP	62	51.149	53.950	9.218	1.00	34.42
ATOM	2611	C	ASP	62	51.020	49.843	9.620	1.00	69.13
ATOM	2612	O	ASP	62	52.212	49.614	9.403	1.00	34.42
ATOM	2613	N	ASP	63	50.219	48.932	10.176	1.00	37.05
ATOM	2615	CA	ASP	63	50.841	47.653	10.476	1.00	37.05
ATOM	2616	CB	ASP	63	50.404	47.047	11.818	1.00	31.00
ATOM	2617	CG	ASP	63	49.130	47.638	12.344	1.00	31.00
ATOM	2618	OD1	ASP	63	49.206	48.353	13.380	1.00	31.00
ATOM	2619	OD2	ASP	63	48.083	47.396	11.705	1.00	31.00
ATOM	2620	C	ASP	63	50.729	46.662	9.365	1.00	37.05
ATOM	2621	O	ASP	63	50.195	45.574	9.558	1.00	31.00
ATOM	2622	N	PHE	64	51.151	47.070	8.179	1.00	9.67
ATOM	2624	CA	PHE	64	51.163	46.178	7.041	1.00	9.67
ATOM	2625	CB	PHE	64	49.824	46.205	6.333	1.00	25.09
ATOM	2626	CG	PHE	64	48.767	45.403	7.020	1.00	25.09
ATOM	2627	CD1	PHE	64	47.897	45.998	7.930	1.00	25.09
ATOM	2628	CD2	PHE	64	48.641	44.050	6.761	1.00	25.09
ATOM	2629	CE1	PHE	64	46.931	45.264	8.573	1.00	25.09
ATOM	2630	CE2	PHE	64	47.666	43.294	7.403	1.00	25.09
ATOM	2631	CZ	PHE	64	46.805	43.902	8.312	1.00	25.09
ATOM	2632	C	PHE	64	52.293	46.600	6.112	1.00	9.67
ATOM	2633	O	PHE	64	52.075	46.831	4.923	1.00	25.09
ATOM	2634	N	LYS	65	53.521	46.632	6.649	1.00	35.36
ATOM	2636	CA	LYS	65	54.705	47.077	5.895	1.00	35.36
ATOM	2637	CB	LYS	65	55.323	48.312	6.556	1.00	32.71
ATOM	2638	CG	LYS	65	54.338	49.329	7.073	1.00	32.71
ATOM	2639	CD	LYS	65	53.444	49.804	5.960	1.00	32.71
ATOM	2640	CE	LYS	65	54.174	50.709	5.006	1.00	32.71
ATOM	2641	NZ	LYS	65	53.726	52.139	5.153	1.00	32.71
ATOM	2645	C	LYS	65	55.847	46.104	5.692	1.00	35.36
ATOM	2646	O	LYS	65	56.414	45.574	6.651	1.00	32.71
ATOM	2647	N	GLY	66	56.262	45.981	4.431	1.00	89.30
ATOM	2649	CA	GLY	66	57.401	45.142	4.072	1.00	89.30
ATOM	2650	C	GLY	66	57.055	44.153	2.973	1.00	89.30
ATOM	2651	O	GLY	66	57.389	44.293	1.781	1.00	46.24

Table 5: Three dimensi nal coordinates of HC - CDR3 (HC: GLU99 - TYR110) from BC2

					x	y	z	Q	B
ATOM	2965	N	GLU	99	35.523	49.858	-3.257	1.00	25.76
ATOM	2967	CA	GLU	99	34.886	51.032	-2.668	1.00	25.76
ATOM	2968	CB	GLU	99	35.928	51.777	-1.791	1.00	63.63
ATOM	2969	CG	GLU	99	35.878	53.373	-1.706	1.00	63.63
ATOM	2970	CD	GLU	99	37.307	54.052	-1.532	1.00	63.63
ATOM	2971	OE1	GLU	99	38.278	53.384	-1.090	1.00	63.63
ATOM	2972	OE2	GLU	99	37.460	55.269	-1.828	1.00	63.63
ATOM	2973	C	GLU	99	34.507	51.829	-3.943	1.00	25.76
ATOM	2974	O	GLU	99	35.321	51.930	-4.866	1.00	63.63
ATOM	2975	N	GLY	100	33.234	52.203	-4.085	1.00	36.41
ATOM	2977	CA	GLY	100	32.814	52.965	-5.257	1.00	36.41
ATOM	2978	C	GLY	100	31.914	54.127	-4.831	1.00	36.41
ATOM	2979	O	GLY	100	31.060	53.923	-3.995	1.00	41.46
ATOM	2980	N	ASN	101	31.966	55.277	-5.502	1.00	33.66
ATOM	2982	CA	ASN	101	31.196	56.434	-5.060	1.00	33.66
ATOM	2983	CB	ASN	101	31.810	57.744	-5.534	1.00	24.12
ATOM	2984	CG	ASN	101	32.059	58.676	-4.388	1.00	24.12
ATOM	2985	OD1	ASN	101	31.122	59.065	-3.700	1.00	24.12
ATOM	2986	ND2	ASN	101	33.320	58.941	-4.099	1.00	24.12
ATOM	2989	C	ASN	101	29.689	56.506	-5.183	1.00	33.66
ATOM	2990	O	ASN	101	29.117	56.182	-6.233	1.00	24.12
ATOM	2991	N	MET	102	29.083	57.024	-4.102	1.00	83.69
ATOM	2993	CA	MET	102	27.625	57.284	-3.908	1.00	83.69
ATOM	2994	CB	MET	102	26.730	56.030	-4.143	1.00	59.11
ATOM	2995	CG	MET	102	25.270	56.204	-3.635	1.00	59.11
ATOM	2996	SD	MET	102	23.981	55.029	-4.261	1.00	59.11
ATOM	2997	CE	MET	102	22.477	56.146	-4.344	1.00	59.11
ATOM	2998	C	MET	102	27.430	57.829	-2.459	1.00	83.69
ATOM	2999	O	MET	102	27.367	57.011	-1.513	1.00	59.11
ATOM	3000	N	ASP	103	27.313	59.177	-2.335	1.00	81.57
ATOM	3002	CA	ASP	103	27.125	59.990	-1.086	1.00	81.57
ATOM	3003	CB	ASP	103	26.625	59.139	0.117	1.00	22.70
ATOM	3004	CG	ASP	103	26.176	59.987	1.343	1.00	22.70
ATOM	3005	OD1	ASP	103	26.907	60.892	1.813	1.00	22.70
ATOM	3006	OD2	ASP	103	25.106	59.666	1.902	1.00	22.70
ATOM	3007	C	ASP	103	28.446	60.681	-0.759	1.00	81.57
ATOM	3008	O	ASP	103	28.961	60.589	0.366	1.00	22.70
ATOM	3009	N	GLY	104	28.984	61.379	-1.761	1.00	86.53
ATOM	3011	CA	GLY	104	30.272	62.065	-1.608	1.00	86.53
ATOM	3012	C	GLY	104	31.473	61.122	-1.460	1.00	86.53
ATOM	3013	O	GLY	104	32.234	60.889	-2.412	1.00	46.20
ATOM	3014	N	TYR	105	31.716	60.669	-0.228	1.00	98.58
ATOM	3016	CA	TYR	105	32.808	59.688	0.036	1.00	98.58
ATOM	3017	CB	TYR	105	33.017	59.412	1.557	1.00	64.10
ATOM	3018	CG	TYR	105	33.326	60.523	2.585	1.00	64.10
ATOM	3019	CD1	TYR	105	34.643	60.884	2.881	1.00	64.10
ATOM	3020	CE1	TYR	105	34.952	61.681	3.977	1.00	64.10
ATOM	3021	CD2	TYR	105	32.318	61.015	3.435	1.00	64.10
ATOM	3022	CE2	TYR	105	32.620	61.810	4.531	1.00	64.10
ATOM	3023	CZ	TYR	105	33.936	62.128	4.802	1.00	64.10
ATOM	3024	OH	TYR	105	34.269	62.843	5.920	1.00	64.10
ATOM	3026	C	TYR	105	32.256	58.342	-0.529	1.00	98.58
ATOM	3027	O	TYR	105	31.153	58.311	-1.096	1.00	64.10
ATOM	3028	N	PHE	106	32.944	57.243	-0.170	1.00	48.28
ATOM	3030	CA	PHE	106	32.570	55.829	-0.484	1.00	48.28
ATOM	3031	CB	PHE	106	32.058	55.183	0.800	1.00	53.07
ATOM	3032	CG	PHE	106	30.689	55.652	1.196	1.00	53.07
ATOM	3033	CD1	PHE	106	30.486	56.963	1.576	1.00	53.07
ATOM	3034	CD2	PHE	106	29.597	54.794	1.117	1.00	53.07
ATOM	3035	CE1	PHE	106	29.255	57.405	1.875	1.00	53.07
ATOM	3036	CE2	PHE	106	28.347	55.232	1.414	1.00	53.07
ATOM	3037	CZ	PHE	106	28.161	56.548	1.791	1.00	53.07
ATOM	3038	C	PHE	106	31.498	55.596	-1.605	1.00	48.28
ATOM	3039	O	PHE	106	31.316	56.481	-2.420	1.00	53.07
ATOM	3040	N	PRO	107	30.807	54.401	-1.651	1.00	76.34
ATOM	3041	CD	PRO	107	29.472	54.859	-2.148	1.00	42.84
ATOM	3042	CA	PRO	107	30.633	53.080	-0.965	1.00	76.34
ATOM	3043	CB	PRO	107	29.321	52.561	-1.567	1.00	42.84
ATOM	3044	CG	PRO	107	28.479	53.811	-1.600	1.00	42.84
ATOM	3045	C	PRO	107	31.730	51.933	-0.822	1.00	76.34

C nt./ Table 5

					x	y	z	Q	B
ATOM	3046	O	PRO	107	32.951	52.163	-0.993	1.00	42.84
ATOM	3047	N	PHE	108	31.227	50.700	-0.638	1.00	52.21
ATOM	3049	CA	PHE	108	31.951	49.437	-0.323	1.00	52.21
ATOM	3050	CB	PHE	108	31.919	49.332	1.174	1.00	28.72
ATOM	3051	CG	PHE	108	30.743	50.065	1.736	1.00	28.72
ATOM	3052	CD1	PHE	108	30.900	51.325	2.267	1.00	28.72
ATOM	3053	CD2	PHE	108	29.464	49.611	1.445	1.00	28.72
ATOM	3054	CE1	PHE	108	29.788	52.112	2.467	1.00	28.72
ATOM	3055	CE2	PHE	108	28.351	50.384	1.636	1.00	28.72
ATOM	3056	CZ	PHE	108	28.508	51.635	2.135	1.00	28.72
ATOM	3057	C	PHE	108	30.973	48.375	-0.826	1.00	52.21
ATOM	3058	O	PHE	108	30.487	47.516	-0.077	1.00	28.72
ATOM	3059	N	THR	109	30.699	48.439	-2.115	1.00	26.26
ATOM	3061	CA	THR	109	29.735	47.613	-2.797	1.00	26.26
ATOM	3062	CB	THR	109	29.620	48.129	-4.186	1.00	36.21
ATOM	3063	OG1	THR	109	30.948	48.431	-4.661	1.00	36.21
ATOM	3065	CG2	THR	109	28.723	49.376	-4.229	1.00	36.21
ATOM	3066	C	THR	109	29.831	46.122	-2.998	1.00	26.26
ATOM	3067	O	THR	109	28.942	45.377	-2.617	1.00	36.21
ATOM	3068	N	TYR	110	30.817	45.735	-3.796	1.00	20.44
ATOM	3070	CA	TYR	110	31.000	44.328	-4.171	1.00	20.44
ATOM	3071	CB	TYR	110	30.912	44.207	-5.686	1.00	60.15
ATOM	3072	CG	TYR	110	29.897	45.158	-6.284	1.00	60.15
ATOM	3073	CD1	TYR	110	28.578	45.154	-5.841	1.00	60.15
ATOM	3074	CE1	TYR	110	27.628	45.978	-6.424	1.00	60.15
ATOM	3075	CD2	TYR	110	30.246	46.025	-7.321	1.00	60.15
ATOM	3076	CE2	TYR	110	29.315	46.848	-7.903	1.00	60.15
ATOM	3077	CZ	TYR	110	27.998	46.822	-7.470	1.00	60.15
ATOM	3078	OH	TYR	110	27.074	47.577	-8.158	1.00	60.15
ATOM	3080	C	TYR	110	32.284	43.665	-3.691	1.00	20.44
ATOM	3081	O	TYR	110	33.283	43.680	-4.404	1.00	60.15

Table 6: Three dimensional coordinates of LC - CDR1 (LC: ARG24 - HIS33) from BC2

					x	y	z	Q	B
ATOM	199	N	ARG	24	31.034	53.669	19.975	1.00	35.70
ATOM	201	CA	ARG	24	31.810	54.840	20.383	1.00	35.70
ATOM	202	CB	ARG	24	32.226	54.801	21.876	1.00	43.83
ATOM	203	CG	ARG	24	31.253	54.267	22.939	1.00	43.83
ATOM	204	CD	ARG	24	31.676	54.727	24.383	1.00	43.83
ATOM	205	NE	ARG	24	33.056	54.377	24.755	1.00	43.83
ATOM	207	CZ	ARG	24	33.426	53.850	25.931	1.00	43.83
ATOM	208	NH1	ARG	24	32.531	53.605	26.891	1.00	43.83
ATOM	211	NH2	ARG	24	34.697	53.526	26.132	1.00	43.83
ATOM	214	C	ARG	24	33.123	54.991	19.621	1.00	35.70
ATOM	215	O	ARG	24	33.959	54.092	19.630	1.00	43.83
ATOM	216	N	ALA	25	33.326	56.123	18.974	1.00	82.87
ATOM	218	CA	ALA	25	34.622	56.346	18.320	1.00	82.87
ATOM	219	CB	ALA	25	34.436	57.225	17.056	1.00	87.02
ATOM	220	C	ALA	25	35.461	57.105	19.369	1.00	82.87
ATOM	221	O	ALA	25	34.882	57.853	20.152	1.00	87.02
ATOM	222	N	SER	26	36.786	56.920	19.422	1.00	44.67
ATOM	224	CA	SER	26	37.565	57.688	20.410	1.00	44.67
ATOM	225	CB	SER	26	39.000	57.177	20.557	1.00	4.82
ATOM	226	OG	SER	26	39.698	57.261	19.336	1.00	4.82
ATOM	228	C	SER	26	37.582	59.186	20.040	1.00	44.67
ATOM	229	O	SER	26	37.708	60.047	20.912	1.00	4.82
ATOM	230	N	SER	27	37.430	59.501	18.755	1.00	27.16
ATOM	232	CA	SER	27	37.462	60.916	18.351	1.00	27.16
ATOM	233	CB	SER	27	38.837	61.282	17.765	1.00	37.32
ATOM	234	OG	SER	27	39.886	61.091	18.724	1.00	37.32
ATOM	236	C	SER	27	36.374	61.225	17.362	1.00	27.16
ATOM	237	O	SER	27	35.718	60.310	16.860	1.00	37.32
ATOM	238	N	SER	28	36.185	62.501	17.060	1.00	32.79
ATOM	240	CA	SER	28	35.117	62.876	16.134	1.00	32.79
ATOM	241	CB	SER	28	34.817	64.378	16.238	1.00	44.89
ATOM	242	OG	SER	28	34.248	64.686	17.509	1.00	44.89
ATOM	244	C	SER	28	35.316	62.487	14.671	1.00	32.79
ATOM	245	O	SER	28	36.334	62.847	14.060	1.00	44.89

Cont./ Table 6

					x	y	z	Q	B
ATOM	246	N	VAL	29	34.333	61.749	14.132	1.00	25.47
ATOM	248	CA	VAL	29	34.322	61.309	12.731	1.00	25.47
ATOM	249	CB	VAL	29	34.592	59.832	12.597	1.00	6.08
ATOM	250	CG1	VAL	29	33.479	59.053	13.249	1.00	6.08
ATOM	251	CG2	VAL	29	34.735	59.486	11.152	1.00	6.08
ATOM	252	C	VAL	29	32.990	61.664	12.049	1.00	25.47
ATOM	253	O	VAL	29	31.974	61.820	12.715	1.00	6.08
ATOM	254	N	ASN	30	32.994	61.694	10.711	1.00	14.73
ATOM	256	CA	ASN	30	31.843	62.139	9.908	1.00	14.73
ATOM	257	CB	ASN	30	32.372	62.765	8.606	1.00	54.87
ATOM	258	CG	ASN	30	33.253	64.006	8.853	1.00	54.87
ATOM	259	OD1	ASN	30	33.627	64.730	7.915	1.00	54.87
ATOM	260	ND2	ASN	30	33.581	64.265	10.123	1.00	54.87
ATOM	263	C	ASN	30	30.530	61.380	9.587	1.00	14.73
ATOM	264	O	ASN	30	29.515	62.046	9.304	1.00	54.87
ATOM	265	N	TYR	31	30.508	60.040	9.619	1.00	32.69
ATOM	267	CA	TYR	31	29.296	59.231	9.272	1.00	32.69
ATOM	268	CB	TYR	31	28.842	59.474	7.827	1.00	35.47
ATOM	269	CG	TYR	31	29.807	58.968	6.782	1.00	35.47
ATOM	270	CD1	TYR	31	29.369	58.639	5.509	1.00	35.47
ATOM	271	CE1	TYR	31	30.253	58.276	4.526	1.00	35.47
ATOM	272	CD2	TYR	31	31.180	58.883	7.021	1.00	35.47
ATOM	273	CE2	TYR	31	32.065	58.497	6.034	1.00	35.47
ATOM	274	CZ	TYR	31	31.597	58.200	4.776	1.00	35.47
ATOM	275	OH	TYR	31	32.441	57.819	3.774	1.00	35.47
ATOM	277	C	TYR	31	29.598	57.764	9.380	1.00	32.69
ATOM	278	O	TYR	31	30.758	57.393	9.362	1.00	35.47
ATOM	279	N	MET	32	28.582	56.902	9.311	1.00	32.43
ATOM	281	CA	MET	32	28.871	55.457	9.421	1.00	32.43
ATOM	282	CB	MET	32	28.762	54.944	10.841	1.00	25.19
ATOM	283	CG	MET	32	30.091	54.566	11.416	1.00	25.19
ATOM	284	SD	MET	32	29.802	53.661	12.911	1.00	25.19
ATOM	285	CE	MET	32	30.987	54.323	14.048	1.00	25.19
ATOM	286	C	MET	32	28.286	54.415	8.494	1.00	32.43
ATOM	287	O	MET	32	27.156	54.486	8.031	1.00	25.19
ATOM	288	N	HIS	33	29.094	53.397	8.266	1.00	41.58
ATOM	290	CA	HIS	33	28.729	52.285	7.411	1.00	41.58
ATOM	291	CB	HIS	33	29.763	52.135	6.303	1.00	27.09
ATOM	292	CG	HIS	33	29.889	53.329	5.438	1.00	27.09
ATOM	293	CD2	HIS	33	28.963	54.054	4.784	1.00	27.09
ATOM	294	ND1	HIS	33	31.084	53.947	5.213	1.00	27.09
ATOM	296	CE1	HIS	33	30.912	55.005	4.445	1.00	27.09
ATOM	297	NE2	HIS	33	29.619	55.085	4.178	1.00	27.09
ATOM	299	C	HIS	33	28.741	51.040	8.265	1.00	41.58
ATOM	300	O	HIS	33	29.751	50.763	8.934	1.00	27.09

Table 7: Three dimensional c rdinates of LC - CDR2 (ALA49 - SER55) from BC2

					x	y	z	Q	B
ATOM	462	N	ALA	49	26.073	55.473	5.034	1.00	33.29
ATOM	464	CA	ALA	49	25.852	56.839	5.537	1.00	33.29
ATOM	465	CB	ALA	49	25.280	57.702	4.416	1.00	20.38
ATOM	466	C	ALA	49	24.957	56.935	6.776	1.00	33.29
ATOM	467	O	ALA	49	23.917	57.578	6.722	1.00	20.38
ATOM	468	N	THR	50	25.356	56.269	7.854	1.00	27.27
ATOM	470	CA	THR	50	24.647	56.254	9.128	1.00	27.27
ATOM	471	CB	THR	50	24.727	57.596	9.824	1.00	38.91
ATOM	472	OG1	THR	50	26.101	57.970	9.914	1.00	38.91
ATOM	474	CG2	THR	50	24.118	57.496	11.237	1.00	38.91
ATOM	475	C	THR	50	23.205	55.813	9.182	1.00	27.27
ATOM	476	O	THR	50	22.882	54.921	9.943	1.00	38.91
ATOM	477	N	SER	51	22.320	56.513	8.481	1.00	17.32
ATOM	479	CA	SER	51	20.912	56.148	8.500	1.00	17.32
ATOM	480	CB	SER	51	20.080	57.295	9.084	1.00	61.11
ATOM	481	OG	SER	51	20.699	57.780	10.281	1.00	61.11
ATOM	483	C	SER	51	20.422	55.717	7.121	1.00	17.32
ATOM	484	O	SER	51	19.258	55.405	6.945	1.00	61.11
ATOM	485	N	ASN	52	21.304	55.713	6.139	1.00	28.10
ATOM	487	CA	ASN	52	20.921	55.255	4.809	1.00	28.10
ATOM	488	CB	ASN	52	21.851	55.873	3.788	1.00	33.84
ATOM	489	CG	ASN	52	21.631	57.348	3.607	1.00	33.84
ATOM	490	OD1	ASN	52	20.881	58.004	4.349	1.00	33.84
ATOM	491	ND2	ASN	52	22.323	57.893	2.620	1.00	33.84
ATOM	494	C	ASN	52	20.954	53.713	4.650	1.00	28.10
ATOM	495	O	ASN	52	22.032	53.113	4.686	1.00	33.84
ATOM	496	N	LEU	53	19.797	53.084	4.392	1.00	46.86
ATOM	498	CA	LEU	53	19.714	51.607	4.228	1.00	46.86
ATOM	499	CB	LEU	53	18.296	51.079	4.477	1.00	14.22
ATOM	500	CG	LEU	53	17.803	51.184	5.911	1.00	14.22
ATOM	501	CD1	LEU	53	16.468	50.481	6.075	1.00	14.22
ATOM	502	CD2	LEU	53	18.826	50.577	6.823	1.00	14.22
ATOM	503	C	LEU	53	20.224	51.072	2.880	1.00	46.86
ATOM	504	O	LEU	53	20.184	51.769	1.857	1.00	14.22
ATOM	505	N	ALA	54	20.731	49.838	2.911	1.00	41.00
ATOM	507	CA	ALA	54	21.272	49.153	1.737	1.00	41.00
ATOM	508	CB	ALA	54	22.309	48.157	2.174	1.00	26.54
ATOM	509	C	ALA	54	20.166	48.465	0.946	1.00	41.00
ATOM	510	O	ALA	54	19.073	48.220	1.460	1.00	26.54
ATOM	511	N	SER	55	20.480	48.052	-0.272	1.00	19.96
ATOM	513	CA	SER	55	19.452	47.470	-1.097	1.00	19.96
ATOM	514	CB	SER	55	19.787	47.612	-2.576	1.00	64.54
ATOM	515	OG	SER	55	18.587	47.553	-3.340	1.00	64.54
ATOM	517	C	SER	55	19.037	46.060	-0.792	1.00	19.96
ATOM	518	O	SER	55	19.652	45.088	-1.257	1.00	64.54

Table 8: Three dimensional coordinates of LC - CDR3 (GLN88 - THR96) from BC2

					x	y	z	Q	B
ATOM	803	N	GLN	88	31.968	50.434	10.331	1.00	11.01
ATOM	805	CA	GLN	88	33.222	50.903	9.776	1.00	11.01
ATOM	806	CB	GLN	88	33.420	50.334	8.398	1.00	23.74
ATOM	807	CG	GLN	88	34.485	50.965	7.564	1.00	23.74
ATOM	808	CD	GLN	88	33.951	51.156	6.176	1.00	23.74
ATOM	809	OE1	GLN	88	32.768	51.520	6.006	1.00	23.74
ATOM	810	NE2	GLN	88	34.780	50.887	5.164	1.00	23.74
ATOM	813	C	GLN	88	33.131	52.420	9.743	1.00	11.01
ATOM	814	O	GLN	88	32.034	52.987	9.802	1.00	23.74
ATOM	815	N	GLN	89	34.289	53.063	9.641	1.00	22.56
ATOM	817	CA	GLN	89	34.453	54.515	9.651	1.00	22.56
ATOM	818	CB	GLN	89	35.447	54.806	10.813	1.00	21.80
ATOM	819	CG	GLN	89	36.354	56.035	10.763	1.00	21.80
ATOM	820	CD	GLN	89	37.702	55.805	10.084	1.00	21.80
ATOM	821	OE1	GLN	89	37.886	56.146	8.907	1.00	21.80
ATOM	822	NE2	GLN	89	38.650	55.247	10.817	1.00	21.80
ATOM	825	C	GLN	89	34.989	54.900	8.266	1.00	22.56
ATOM	826	O	GLN	89	35.529	54.045	7.606	1.00	21.80
ATOM	827	N	TRP	90	34.781	56.120	7.772	1.00	27.74
ATOM	829	CA	TRP	90	35.345	56.493	6.449	1.00	27.74
ATOM	830	CB	TRP	90	34.369	56.131	5.308	1.00	90.21
ATOM	831	CG	TRP	90	34.940	55.660	3.942	1.00	90.21
ATOM	832	CD2	TRP	90	35.677	56.438	3.003	1.00	90.21
ATOM	833	CE2	TRP	90	35.840	55.671	1.829	1.00	90.21
ATOM	834	CE3	TRP	90	36.214	57.722	3.022	1.00	90.21
ATOM	835	CD1	TRP	90	34.714	54.453	3.320	1.00	90.21
ATOM	836	NE1	TRP	90	35.249	54.456	2.041	1.00	90.21
ATOM	838	CZ2	TRP	90	36.510	56.156	0.702	1.00	90.21
ATOM	839	CZ3	TRP	90	36.884	58.194	1.890	1.00	90.21
ATOM	840	CH2	TRP	90	37.019	57.413	0.752	1.00	90.21
ATOM	841	C	TRP	90	35.614	57.999	6.437	1.00	27.74
ATOM	842	O	TRP	90	34.962	58.721	5.694	1.00	90.21
ATOM	843	N	SER	91	36.590	58.456	7.236	1.00	33.90
ATOM	845	CA	SER	91	36.919	59.882	7.305	1.00	33.90
ATOM	846	CB	SER	91	35.972	60.566	8.290	1.00	33.23
ATOM	847	OG	SER	91	34.617	60.159	8.093	1.00	33.23
ATOM	849	C	SER	91	38.345	60.167	7.787	1.00	33.90
ATOM	850	O	SER	91	38.725	61.333	7.955	1.00	33.23
ATOM	851	N	ILE	92	39.144	59.128	7.999	1.00	2.00
ATOM	853	CA	ILE	92	40.460	59.355	8.562	1.00	2.00
ATOM	854	CB	ILE	92	40.486	58.910	10.044	1.00	6.47
ATOM	855	CG2	ILE	92	41.380	59.809	10.888	1.00	6.47
ATOM	856	CG1	ILE	92	39.063	58.849	10.607	1.00	6.47
ATOM	857	CD1	ILE	92	38.423	60.168	10.911	1.00	6.47
ATOM	858	C	ILE	92	41.495	58.514	7.947	1.00	2.00
ATOM	859	O	ILE	92	41.199	57.590	7.204	1.00	6.47
ATOM	860	N	ASN	93	42.732	58.864	8.266	1.00	50.27
ATOM	862	CA	ASN	93	43.854	58.038	7.897	1.00	50.27
ATOM	863	CB	ASN	93	45.208	58.800	7.682	1.00	86.79
ATOM	864	CG	ASN	93	46.486	57.828	7.455	1.00	86.79
ATOM	865	OD1	ASN	93	47.427	57.772	8.308	1.00	86.79
ATOM	866	ND2	ASN	93	46.515	57.093	6.321	1.00	86.79
ATOM	869	C	ASN	93	43.951	57.245	9.226	1.00	50.27
ATOM	870	O	ASN	93	43.982	57.844	10.306	1.00	86.79
ATOM	871	N	PRO	94	43.557	55.965	9.198	1.00	31.00
ATOM	872	CD	PRO	94	44.264	54.985	10.018	1.00	20.78
ATOM	873	CA	PRO	94	43.071	55.322	7.987	1.00	31.00
ATOM	874	CB	PRO	94	43.911	54.060	7.900	1.00	20.78
ATOM	875	CG	PRO	94	45.051	54.288	8.974	1.00	20.78
ATOM	876	C	PRO	94	41.636	55.034	8.421	1.00	31.00
ATOM	877	O	PRO	94	41.243	55.377	9.550	1.00	20.78
ATOM	878	N	ARG	95	40.833	54.492	7.530	1.00	12.98
ATOM	880	CA	ARG	95	39.478	54.164	7.925	1.00	12.98
ATOM	881	CB	ARG	95	38.592	54.022	6.711	1.00	25.66
ATOM	882	CG	ARG	95	39.316	53.550	5.504	1.00	25.66
ATOM	883	CD	ARG	95	38.629	54.020	4.254	1.00	25.66
ATOM	884	NE	ARG	95	39.628	54.435	3.283	1.00	25.66
ATOM	886	CZ	ARG	95	39.431	54.489	1.973	1.00	25.66
ATOM	887	NH1	ARG	95	38.274	54.150	1.454	1.00	25.66
ATOM	890	NH2	ARG	95	40.412	54.885	1.183	1.00	25.66
ATOM	893	C	ARG	95	39.599	52.868	8.709	1.00	12.98
ATOM	894	O	ARG	95	40.633	52.213	8.651	1.00	25.66
ATOM	895	N	THR	96	38.605	52.532	9.520	1.00	14.80

Cont./Table 8

ATOM	898	CB	THR	96	39.459	51.542	11.670	1.00	36.32
ATOM	899	OG1	THR	96	38.718	52.498	12.439	1.00	36.32
ATOM	901	CG2	THR	96	40.908	52.045	11.476	1.00	36.32
ATOM	902	C	THR	96	37.365	50.730	10.607	1.00	14.80
ATOM	903	O	THR	96	36.340	51.326	10.292	1.00	36.32

Table 9: Three dimensional coordinates of HC - CDR1 (ASN31 - ASN35) from SB249417

ATOM	2300	N	ASN	31	53.647	23.490	34.881	1.00	20.53
ATOM	2302	CA	ASN	31	54.400	24.257	33.887	1.00	20.53
ATOM	2303	CB	ASN	31	53.820	25.666	33.715	1.00	39.50
ATOM	2304	CG	ASN	31	53.118	25.859	32.376	1.00	39.50
ATOM	2305	OD1	ASN	31	53.469	25.236	31.370	1.00	39.50
ATOM	2306	ND2	ASN	31	52.128	26.741	32.358	1.00	39.50
ATOM	2309	C	ASN	31	55.860	24.369	34.306	1.00	20.53
ATOM	2310	O	ASN	31	56.746	24.530	33.466	1.00	39.50
ATOM	2311	N	TYR	32	56.103	24.314	35.612	1.00	18.56
ATOM	2313	CA	TYR	32	57.458	24.408	36.148	1.00	18.56
ATOM	2314	CB	TYR	32	57.571	25.582	37.122	1.00	41.90
ATOM	2315	CG	TYR	32	57.374	26.943	36.499	1.00	41.90
ATOM	2316	CD1	TYR	32	56.107	27.516	36.415	1.00	41.90
ATOM	2317	CE1	TYR	32	55.923	28.782	35.869	1.00	41.90
ATOM	2318	CD2	TYR	32	58.459	27.672	36.018	1.00	41.90
ATOM	2319	CE2	TYR	32	58.288	28.940	35.472	1.00	41.90
ATOM	2320	CZ	TYR	32	57.017	29.489	35.402	1.00	41.90
ATOM	2321	OH	TYR	32	56.836	30.745	34.875	1.00	41.90
ATOM	2323	C	TYR	32	57.824	23.124	36.875	1.00	18.56
ATOM	2324	O	TYR	32	57.024	22.590	37.642	1.00	41.90
ATOM	2325	N	GLY	33	59.032	22.631	36.626	1.00	32.09
ATOM	2327	CA	GLY	33	59.480	21.415	37.276	1.00	32.09
ATOM	2328	C	GLY	33	59.805	21.659	38.736	1.00	32.09
ATOM	2329	O	GLY	33	60.028	22.802	39.140	1.00	20.56
ATOM	2330	N	MET	34	59.813	20.593	39.530	1.00	8.75
ATOM	2332	CA	MET	34	60.119	20.700	40.949	1.00	8.75
ATOM	2333	CB	MET	34	58.988	20.101	41.787	1.00	26.05
ATOM	2334	CG	MET	34	59.129	20.334	43.283	1.00	26.05
ATOM	2335	SD	MET	34	59.069	22.082	43.705	1.00	26.05
ATOM	2336	CE	MET	34	57.315	22.344	43.849	1.00	26.05
ATOM	2337	C	MET	34	61.417	19.972	41.256	1.00	8.75
ATOM	2338	O	MET	34	61.514	18.759	41.073	1.00	26.05
ATOM	2339	N	ASN	35	62.425	20.722	41.687	1.00	25.14
ATOM	2341	CA	ASN	35	63.720	20.147	42.034	1.00	25.14
ATOM	2342	CB	ASN	35	64.859	21.091	41.642	1.00	22.15
ATOM	2343	CG	ASN	35	65.135	21.097	40.156	1.00	22.15
ATOM	2344	OD1	ASN	35	65.207	22.152	39.533	1.00	22.15
ATOM	2345	ND2	ASN	35	65.347	19.921	39.588	1.00	22.15
ATOM	2348	C	ASN	35	63.785	19.906	43.533	1.00	25.14
ATOM	2349	O	ASN	35	63.256	20.693	44.316	1.00	22.15

Table 10: Three dimensional coordinates of HC-CDR2 (TRP50-GLY66) from SB 249417

ATOM	2490	N	TRP	50	64.690	15.841	39.634	1.00	10.37
ATOM	2492	CA	TRP	50	63.706	16.753	39.073	1.00	10.37
ATOM	2493	CB	TRP	50	64.255	17.405	37.796	1.00	82.57
ATOM	2494	CG	TRP	50	64.648	16.439	36.697	1.00	82.57
ATOM	2495	CD2	TRP	50	64.574	16.669	35.282	1.00	82.57
ATOM	2496	CE2	TRP	50	65.053	15.504	34.643	1.00	82.57
ATOM	2497	CE3	TRP	50	64.150	17.748	34.494	1.00	82.57
ATOM	2498	CD1	TRP	50	65.155	15.177	36.849	1.00	82.57
ATOM	2499	NE1	TRP	50	65.400	14.610	35.622	1.00	82.57
ATOM	2501	CZ2	TRP	50	65.121	15.386	33.249	1.00	82.57
ATOM	2502	CZ3	TRP	50	64.219	17.629	33.106	1.00	82.57
ATOM	2503	CH2	TRP	50	64.701	16.456	32.501	1.00	82.57
ATOM	2504	C	TRP	50	62.412	16.021	38.760	1.00	10.37
ATOM	2505	O	TRP	50	62.403	14.800	38.616	1.00	82.57
ATOM	2506	N	ILE	51	61.315	16.766	38.728	1.00	26.53
ATOM	2508	CA	ILE	51	60.001	16.222	38.405	1.00	26.53
ATOM	2509	CB	ILE	51	59.025	16.284	39.603	1.00	25.59
ATOM	2510	CG2	ILE	51	57.689	15.659	39.225	1.00	25.59
ATOM	2511	CG1	ILE	51	59.599	15.545	40.810	1.00	25.59
ATOM	2512	CD1	ILE	51	58.687	15.577	42.024	1.00	25.59
ATOM	2513	C	ILE	51	59.476	17.151	37.319	1.00	26.53
ATOM	2514	O	ILE	51	59.386	18.359	37.531	1.00	25.59
ATOM	2515	N	ASN	52	59.153	16.601	36.155	1.00	46.03
ATOM	2517	CA	ASN	52	58.651	17.415	35.047	1.00	46.03
ATOM	2518	CB	ASN	52	58.528	16.569	33.783	1.00	45.75
ATOM	2519	CG	ASN	52	58.447	17.406	32.528	1.00	45.75
ATOM	2520	OD1	ASN	52	57.625	18.311	32.421	1.00	45.75
ATOM	2521	ND2	ASN	52	59.298	17.097	31.561	1.00	45.75
ATOM	2524	C	ASN	52	57.300	18.040	35.377	1.00	46.03
ATOM	2525	O	ASN	52	56.899	19.032	34.768	1.00	45.75
ATOM	2526	N	THR	53	56.605	17.449	36.343	1.00	38.29
ATOM	2528	CA	THR	53	55.293	17.917	36.778	1.00	38.29
ATOM	2529	CB	THR	53	55.272	19.452	37.009	1.00	46.19
ATOM	2530	OG1	THR	53	56.181	19.781	38.067	1.00	46.19
ATOM	2532	CG2	THR	53	53.880	19.924	37.393	1.00	46.19
ATOM	2533	C	THR	53	54.194	17.476	35.812	1.00	38.29
ATOM	2534	O	THR	53	53.298	16.727	36.203	1.00	46.19
ATOM	2535	N	ARG	54	54.265	17.906	34.555	1.00	53.63
ATOM	2537	CA	ARG	54	53.261	17.500	33.573	1.00	53.63
ATOM	2538	CB	ARG	54	53.359	18.345	32.298	1.00	31.29
ATOM	2539	CG	ARG	54	54.717	18.334	31.631	1.00	31.29
ATOM	2540	CD	ARG	54	54.742	19.227	30.409	1.00	31.29
ATOM	2541	NE	ARG	54	56.062	19.229	29.782	1.00	31.29
ATOM	2543	CZ	ARG	54	56.666	20.315	29.312	1.00	31.29
ATOM	2544	NH1	ARG	54	56.071	21.499	29.396	1.00	31.29
ATOM	2547	NH2	ARG	54	57.871	20.218	28.766	1.00	31.29
ATOM	2550	C	ARG	54	53.457	16.013	33.267	1.00	53.63
ATOM	2551	O	ARG	54	54.507	15.603	32.771	1.00	31.29
ATOM	2552	N	ASN	55	52.477	15.208	33.670	1.00	58.18
ATOM	2554	CA	ASN	55	52.500	13.754	33.486	1.00	58.18
ATOM	2555	CB	ASN	55	52.879	13.373	32.044	1.00	44.20
ATOM	2556	CG	ASN	55	52.809	11.870	31.785	1.00	44.20
ATOM	2557	OD1	ASN	55	53.602	11.326	31.017	1.00	44.20
ATOM	2558	ND2	ASN	55	51.847	11.197	32.411	1.00	44.20
ATOM	2561	C	ASN	55	53.462	13.105	34.481	1.00	58.18
ATOM	2562	O	ASN	55	53.658	11.888	34.468	1.00	44.20
ATOM	2563	N	GLY	56	54.013	13.916	35.381	1.00	35.82
ATOM	2565	CA	GLY	56	54.947	13.406	36.370	1.00	35.82
ATOM	2566	C	GLY	56	56.103	12.672	35.723	1.00	35.82
ATOM	2567	O	GLY	56	56.637	11.715	36.281	1.00	33.62
ATOM	2568	N	LYS	57	56.477	13.118	34.529	1.00	56.46
ATOM	2570	CA	LYS	57	57.571	12.505	33.790	1.00	56.46
ATOM	2571	CB	LYS	57	57.305	12.584	32.281	1.00	42.16
ATOM	2572	CG	LYS	57	57.015	13.984	31.749	1.00	42.16
ATOM	2573	CD	LYS	57	56.585	13.927	30.289	1.00	42.16
ATOM	2574	CE	LYS	57	56.184	15.294	29.747	1.00	42.16
ATOM	2575	NZ	LYS	57	57.344	16.189	29.495	1.00	42.16
ATOM	2579	C	LYS	57	58.900	13.160	34.138	1.00	56.46
ATOM	2580	O	LYS	57	58.987	13.933	35.098	1.00	42.16
ATOM	2581	N	SER	58	59.930	12.832	33.361	1.00	69.70
ATOM	2583	CA	SER	58	61.273	13.374	33.548	1.00	69.70
ATOM	2584	CB	SER	58	61.377	14.767	32.920	1.00	51.34
ATOM	2585	OG	SER	58	61.034	14.740	31.541	1.00	51.34
ATOM	2587	C	SER	58	61.679	13.421	35.016	1.00	69.70
ATOM	2588	O	SER	58	61.711	14.489	35.631	1.00	51.34
ATOM	2589	N	THR	59	61.928	12.245	35.578	1.00	66.55
ATOM	2591	CA	THR	59	62.336	12.118	36.969	1.00	66.55
ATOM	2592	CB	THR	59	61.465	11.076	37.702	1.00	41.34
ATOM	2593	OG1	THR	59	60.280	10.821	36.937	1.00	41.34

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ATOM	2595	CG2	THR	59	61.058	11.594	39.066	1.00 41.34
ATOM	2596	C	THR	59	63.774	11.622	36.924	1.00 66.55
ATOM	2597	O	THR	59	64.129	10.848	36.029	1.00 41.34
ATOM	2598	N	TYR	60	64.621	12.091	37.835	1.00 40.30
ATOM	2600	CA	TYR	60	66.002	11.629	37.823	1.00 40.30
ATOM	2601	CB	TYR	60	66.869	12.381	38.835	1.00 68.57
ATOM	2602	CG	TYR	60	68.285	11.842	38.911	1.00 68.57
ATOM	2603	CD1	TYR	60	68.980	11.483	37.755	1.00 68.57
ATOM	2604	CE1	TYR	60	70.255	10.929	37.821	1.00 68.57
ATOM	2605	CD2	TYR	60	68.910	11.639	40.137	1.00 68.57
ATOM	2606	CE2	TYR	60	70.186	11.087	40.214	1.00 68.57
ATOM	2607	CZ	TYR	60	70.852	10.734	39.055	1.00 68.57
ATOM	2608	OH	TYR	60	72.108	10.181	39.136	1.00 68.57
ATOM	2610	C	TYR	60	66.035	10.136	38.119	1.00 40.30
ATOM	2611	O	TYR	60	65.463	9.683	39.106	1.00 68.57
ATOM	2612	N	VAL	61	66.720	9.387	37.258	1.00 78.68
ATOM	2614	CA	VAL	61	66.857	7.935	37.386	1.00 78.68
ATOM	2615	CB	VAL	61	67.864	7.381	36.341	1.00 61.99
ATOM	2616	CG1	VAL	61	67.881	5.852	36.363	1.00 61.99
ATOM	2617	CG2	VAL	61	67.518	7.891	34.945	1.00 61.99
ATOM	2618	C	VAL	61	67.323	7.531	38.788	1.00 78.68
ATOM	2619	O	VAL	61	67.113	6.396	39.218	1.00 61.99
ATOM	2620	N	ASP	62	67.955	8.468	39.491	1.00 56.17
ATOM	2622	CA	ASP	62	68.455	8.234	40.840	1.00 56.17
ATOM	2623	CB	ASP	62	67.298	7.887	41.784	1.00 45.87
ATOM	2624	CG	ASP	62	66.192	8.938	41.764	1.00 45.87
ATOM	2625	OD1	ASP	62	66.499	10.131	41.559	1.00 45.87
ATOM	2626	OD2	ASP	62	65.009	8.573	41.936	1.00 45.87
ATOM	2627	C	ASP	62	69.511	7.134	40.810	1.00 56.17
ATOM	2628	O	ASP	62	69.207	5.953	40.977	1.00 45.87
ATOM	2629	N	ASP	63	70.755	7.543	40.574	1.00 73.06
ATOM	2631	CA	ASP	63	71.885	6.623	40.492	1.00 73.06
ATOM	2632	CB	ASP	63	73.194	7.404	40.344	1.00 43.18
ATOM	2633	CG	ASP	63	73.946	7.051	39.072	1.00 43.18
ATOM	2634	OD1	ASP	63	73.828	5.897	38.604	1.00 43.18
ATOM	2635	OD2	ASP	63	74.667	7.924	38.546	1.00 43.18
ATOM	2636	C	ASP	63	71.972	5.697	41.696	1.00 73.06
ATOM	2637	O	ASP	63	72.399	6.110	42.776	1.00 43.18
ATOM	2638	N	PHE	64	71.509	4.461	41.515	1.00 77.35
ATOM	2640	CA	PHE	64	71.521	3.437	42.562	1.00 77.35
ATOM	2641	CB	PHE	64	72.948	3.202	43.071	1.00 68.41
ATOM	2642	CG	PHE	64	73.486	1.836	42.762	1.00 68.41
ATOM	2643	CD1	PHE	64	73.432	1.328	41.467	1.00 68.41
ATOM	2644	CD2	PHE	64	74.047	1.053	43.766	1.00 68.41
ATOM	2645	CE1	PHE	64	73.930	0.058	41.177	1.00 68.41
ATOM	2646	CE2	PHE	64	74.548	-0.219	43.485	1.00 68.41
ATOM	2647	CZ	PHE	64	74.489	-0.717	42.188	1.00 68.41
ATOM	2648	C	PHE	64	70.592	3.723	43.740	1.00 77.35
ATOM	2649	O	PHE	64	70.141	2.795	44.419	1.00 68.41
ATOM	2650	N	LYS	65	70.284	4.996	43.967	1.00 77.80
ATOM	2652	CA	LYS	65	69.414	5.395	45.066	1.00 77.80
ATOM	2653	CB	LYS	65	69.749	6.824	45.525	1.00 59.28
ATOM	2654	CG	LYS	65	71.243	7.133	45.654	1.00 59.28
ATOM	2655	CD	LYS	65	72.017	6.042	46.394	1.00 59.28
ATOM	2656	CE	LYS	65	71.576	5.890	47.841	1.00 59.28
ATOM	2657	NZ	LYS	65	72.374	4.831	48.536	1.00 59.28
ATOM	2661	C	LYS	65	67.940	5.296	44.675	1.00 77.80
ATOM	2662	O	LYS	65	67.188	6.271	44.781	1.00 59.28
ATOM	2663	N	GLY	66	67.523	4.105	44.255	1.00 33.49
ATOM	2665	CA	GLY	66	66.141	3.893	43.863	1.00 33.49
ATOM	2666	C	GLY	66	65.248	3.671	45.067	1.00 33.49
ATOM	2667	O	GLY	66	64.479	2.710	45.117	1.00 26.03

Table 11: Three dimensional coordinates of HC - CDR3 (GLU99 - TYR110) from SB249417

ATOM	2507	N	GLU	99	61.719	25.581	38.831	1.00	50.46
ATOM	2508	CA	GLU	99	62.445	25.725	37.560	1.00	50.46
ATOM	2509	CB	GLU	99	63.093	27.110	37.435	1.00	52.10
ATOM	2510	CG	GLU	99	62.109	28.216	37.059	1.00	52.10
ATOM	2511	CD	GLU	99	62.112	29.390	38.028	1.00	52.10
ATOM	2512	OE1	GLU	99	61.436	30.397	37.735	1.00	52.10
ATOM	2513	OE2	GLU	99	62.772	29.310	39.086	1.00	52.10
ATOM	2514	C	GLU	99	63.461	24.618	37.297	1.00	50.46
ATOM	2515	O	GLU	99	63.484	23.616	38.010	1.00	52.10
ATOM	2516	N	GLY	100	64.259	24.775	36.242	1.00	42.17
ATOM	2517	CA	GLY	100	65.249	23.764	35.914	1.00	42.17
ATOM	2518	C	GLY	100	66.331	24.192	34.937	1.00	42.17
ATOM	2519	O	GLY	100	66.089	24.997	34.033	1.00	27.11
ATOM	2520	N	ASN	101	67.526	23.635	35.132	1.00	59.61
ATOM	2521	CA	ASN	101	68.704	23.902	34.306	1.00	59.61
ATOM	2522	CB	ASN	101	68.654	23.089	33.006	1.00	55.09
ATOM	2523	CG	ASN	101	68.926	21.612	33.229	1.00	55.09
ATOM	2524	OD1	ASN	101	68.323	20.985	34.102	1.00	55.09
ATOM	2525	ND2	ASN	101	69.834	21.046	32.439	1.00	55.09
ATOM	2528	C	ASN	101	68.940	25.379	34.011	1.00	59.61
ATOM	2529	O	ASN	101	69.643	26.062	34.763	1.00	55.09
ATOM	2530	N	MET	102	68.369	25.867	32.914	1.00	51.25
ATOM	2531	CA	MET	102	68.514	27.265	32.530	1.00	51.25
ATOM	2532	CB	MET	102	69.931	27.556	32.037	1.00	39.15
ATOM	2533	CG	MET	102	70.367	29.002	32.229	1.00	39.15
ATOM	2534	SD	MET	102	69.099	30.248	31.922	1.00	39.15
ATOM	2535	CE	MET	102	69.132	31.094	33.482	1.00	39.15
ATOM	2536	C	MET	102	67.519	27.571	31.424	1.00	51.25
ATOM	2537	O	MET	102	67.866	27.577	30.241	1.00	39.15
ATOM	2538	N	ASP	103	66.270	27.787	31.814	1.00	52.39
ATOM	2539	CA	ASP	103	65.210	28.095	30.867	1.00	52.39
ATOM	2540	CB	ASP	103	64.309	26.865	30.664	1.00	81.62
ATOM	2541	CG	ASP	103	65.099	25.592	30.350	1.00	81.62
ATOM	2542	OD1	ASP	103	64.784	24.533	30.939	1.00	81.62
ATOM	2543	OD2	ASP	103	66.028	25.642	29.514	1.00	81.62
ATOM	2544	C	ASP	103	64.391	29.250	31.440	1.00	52.39
ATOM	2545	O	ASP	103	64.181	29.324	32.653	1.00	81.62
ATOM	2546	N	GLY	104	63.980	30.176	30.577	1.00	38.36
ATOM	2547	CA	GLY	104	63.181	31.309	31.019	1.00	38.36
ATOM	2548	C	GLY	104	63.874	32.286	31.954	1.00	38.36
ATOM	2549	O	GLY	104	63.209	33.068	32.630	1.00	35.81
ATOM	2550	N	TYR	105	65.204	32.221	32.005	1.00	78.70
ATOM	2551	CA	TYR	105	66.028	33.098	32.843	1.00	78.70
ATOM	2552	CB	TYR	105	66.298	34.426	32.125	1.00	41.71
ATOM	2553	CG	TYR	105	67.726	34.593	31.653	1.00	41.71
ATOM	2554	CD1	TYR	105	68.492	33.493	31.266	1.00	41.71
ATOM	2555	CE1	TYR	105	69.812	33.644	30.838	1.00	41.71
ATOM	2556	CD2	TYR	105	68.315	35.854	31.599	1.00	41.71
ATOM	2557	CE2	TYR	105	69.632	36.017	31.172	1.00	41.71
ATOM	2558	CZ	TYR	105	70.372	34.910	30.794	1.00	41.71
ATOM	2559	OH	TYR	105	71.671	35.077	30.382	1.00	41.71
ATOM	2560	C	TYR	105	65.515	33.355	34.263	1.00	78.70
ATOM	2561	O	TYR	105	65.349	34.503	34.679	1.00	41.71
ATOM	2562	N	PHE	106	65.297	32.275	35.006	1.00	53.79
ATOM	2563	CA	PHE	106	64.815	32.362	36.381	1.00	53.79
ATOM	2564	CB	PHE	106	63.302	32.606	36.355	1.00	64.88
ATOM	2565	CG	PHE	106	62.867	33.837	37.093	1.00	64.88
ATOM	2566	CD1	PHE	106	63.142	35.104	36.586	1.00	64.88
ATOM	2567	CD2	PHE	106	62.162	33.732	38.286	1.00	64.88
ATOM	2568	CE1	PHE	106	62.722	36.246	37.255	1.00	64.88
ATOM	2569	CE2	PHE	106	61.736	34.868	38.964	1.00	64.88
ATOM	2570	CZ	PHE	106	62.016	36.129	38.447	1.00	64.88
ATOM	2571	C	PHE	106	65.099	31.140	37.282	1.00	53.79
ATOM	2572	O	PHE	106	64.552	31.055	38.381	1.00	64.88
ATOM	2573	N	PRO	107	66.005	30.221	36.878	1.00	52.80
ATOM	2574	CD	PRO	107	66.836	30.142	35.667	1.00	42.34
ATOM	2575	CA	PRO	107	66.268	29.051	37.725	1.00	52.80
ATOM	2576	CB	PRO	107	67.393	28.338	36.977	1.00	42.34
ATOM	2577	CG	PRO	107	67.103	28.666	35.568	1.00	42.34
ATOM	2578	C	PRO	107	66.623	29.241	39.198	1.00	52.80
ATOM	2579	O	PRO	107	67.275	30.212	39.596	1.00	42.34
ATOM	2580	N	PHE	108	66.199	28.252	39.980	1.00	39.89
ATOM	2581	CA	PHE	108	66.421	28.160	41.417	1.00	39.89
ATOM	2582	CB	PHE	108	67.823	27.639	41.713	1.00	29.53

Cont./Table 11

ATOM	2583	CG	PHE	108	67.986	26.177	41.417	1.00	29.53
ATOM	2584	CD1	PHE	108	67.950	25.711	40.107	1.00	29.53
ATOM	2585	CD2	PHE	108	68.127	25.258	42.450	1.00	29.53
ATOM	2586	CE1	PHE	108	68.049	24.350	39.833	1.00	29.53
ATOM	2587	CE2	PHE	108	68.228	23.894	42.186	1.00	29.53
ATOM	2588	CZ	PHE	108	68.188	23.440	40.878	1.00	29.53
ATOM	2589	C	PHE	108	66.057	29.348	42.287	1.00	39.89
ATOM	2590	O	PHE	108	66.654	29.578	43.342	1.00	29.53
ATOM	2591	N	THR	109	65.082	30.115	41.821	1.00	37.60
ATOM	2592	CA	THR	109	64.572	31.243	42.571	1.00	37.60
ATOM	2593	CB	THR	109	64.110	32.374	41.638	1.00	39.99
ATOM	2594	OG1	THR	109	63.235	31.842	40.638	1.00	39.99
ATOM	2595	CG2	THR	109	65.303	33.016	40.950	1.00	39.99
ATOM	2596	C	THR	109	63.369	30.609	43.267	1.00	37.60
ATOM	2597	O	THR	109	62.694	29.761	42.676	1.00	39.99
ATOM	2598	N	TYR	110	63.113	30.999	44.511	1.00	23.43
ATOM	2599	CA	TYR	110	62.006	30.449	45.292	1.00	23.43
ATOM	2600	CB	TYR	110	60.701	30.367	44.481	1.00	42.41
ATOM	2601	CG	TYR	110	60.156	31.673	43.951	1.00	42.41
ATOM	2602	CD1	TYR	110	60.138	31.931	42.583	1.00	42.41
ATOM	2603	CE1	TYR	110	59.587	33.104	42.077	1.00	42.41
ATOM	2604	CD2	TYR	110	59.611	32.628	44.807	1.00	42.41
ATOM	2605	CE2	TYR	110	59.055	33.807	44.309	1.00	42.41
ATOM	2606	CZ	TYR	110	59.047	34.035	42.942	1.00	42.41
ATOM	2607	OH	TYR	110	58.484	35.185	42.439	1.00	42.41
ATOM	2608	C	TYR	110	62.358	29.042	45.763	1.00	23.43
ATOM	2609	O	TYR	110	62.436	28.111	44.960	1.00	42.41

Table 12: Three dimensional coordinates of LC-CDR1 (ARG24-HIS33) from SB249417

ATOM	161	N	ARG	24	85.923	25.430	39.568	1.00	40.61
ATOM	162	CA	ARG	24	86.364	24.572	38.468	1.00	40.61
ATOM	163	CB	ARG	24	87.477	23.636	38.953	1.00	54.47
ATOM	164	CG	ARG	24	88.672	23.525	38.021	1.00	54.47
ATOM	165	CD	ARG	24	89.786	24.476	38.433	1.00	54.47
ATOM	166	NE	ARG	24	89.329	25.861	38.511	1.00	54.47
ATOM	167	CZ	ARG	24	90.019	26.850	39.069	1.00	54.47
ATOM	168	NH1	ARG	24	91.212	26.619	39.605	1.00	54.47
ATOM	171	NH2	ARG	24	89.510	28.073	39.101	1.00	54.47
ATOM	174	C	ARG	24	85.191	23.729	37.974	1.00	40.61
ATOM	175	O	ARG	24	84.258	23.455	38.735	1.00	54.47
ATOM	176	N	ALA	25	85.251	23.296	36.718	1.00	33.05
ATOM	177	CA	ALA	25	84.185	22.475	36.146	1.00	33.05
ATOM	178	CB	ALA	25	83.270	23.332	35.275	1.00	58.44
ATOM	179	C	ALA	25	84.702	21.278	35.348	1.00	33.05
ATOM	180	O	ALA	25	83.923	20.409	34.958	1.00	58.44
ATOM	181	N	SER	26	86.006	21.249	35.087	1.00	57.44
ATOM	182	CA	SER	26	86.641	20.165	34.330	1.00	57.44
ATOM	183	CB	SER	26	86.518	18.828	35.080	1.00	65.59
ATOM	184	OG	SER	26	87.351	17.828	34.505	1.00	65.59
ATOM	185	C	SER	26	86.093	20.030	32.903	1.00	57.44
ATOM	186	O	SER	26	86.698	20.533	31.952	1.00	65.59
ATOM	187	N	SER	27	84.946	19.366	32.762	1.00	55.02
ATOM	188	CA	SER	27	84.317	19.158	31.459	1.00	55.02
ATOM	189	CB	SER	27	82.987	18.420	31.627	1.00	53.39
ATOM	190	OG	SER	27	83.183	17.167	32.259	1.00	53.39
ATOM	191	C	SER	27	84.091	20.476	30.725	1.00	55.02
ATOM	192	O	SER	27	84.718	20.717	29.690	1.00	53.39
ATOM	193	N	SER	28	83.232	21.316	31.307	1.00	33.90
ATOM	194	CA	SER	28	82.834	22.647	30.825	1.00	33.90
ATOM	195	CB	SER	28	83.830	23.274	29.833	1.00	57.68
ATOM	196	OG	SER	28	83.804	22.660	28.552	1.00	57.68
ATOM	197	C	SER	28	81.430	22.670	30.238	1.00	33.90
ATOM	198	O	SER	28	81.089	21.866	29.368	1.00	57.68
ATOM	199	N	VAL	29	80.619	23.592	30.742	1.00	39.14
ATOM	200	CA	VAL	29	79.244	23.773	30.294	1.00	39.14
ATOM	201	CB	VAL	29	78.226	23.123	31.278	1.00	50.11
ATOM	202	CG1	VAL	29	78.394	21.612	31.295	1.00	50.11
ATOM	203	CG2	VAL	29	78.401	23.688	32.681	1.00	50.11
ATOM	204	C	VAL	29	79.031	25.282	30.251	1.00	39.14
ATOM	205	O	VAL	29	79.981	26.036	30.028	1.00	50.11
ATOM	206	N	ASN	30	77.798	25.731	30.449	1.00	34.36
ATOM	207	CA	ASN	30	77.518	27.157	30.446	1.00	34.36
ATOM	208	CB	ASN	30	77.105	27.633	29.051	1.00	69.95
ATOM	209	CG	ASN	30	77.315	29.129	28.859	1.00	69.95
ATOM	210	OD1	ASN	30	76.945	29.938	29.712	1.00	69.95
ATOM	211	ND2	ASN	30	77.935	29.501	27.744	1.00	69.95
ATOM	214	C	ASN	30	76.405	27.416	31.437	1.00	34.36
ATOM	215	O	ASN	30	75.668	26.496	31.799	1.00	69.95
ATOM	216	N	TYR	31	76.313	28.662	31.895	1.00	51.94
ATOM	217	CA	TYR	31	75.299	29.094	32.853	1.00	51.94
ATOM	218	CB	TYR	31	73.896	28.690	32.379	1.00	66.29
ATOM	219	CG	TYR	31	73.464	29.386	31.105	1.00	66.29
ATOM	220	CD1	TYR	31	72.980	28.661	30.016	1.00	66.29
ATOM	221	CE1	TYR	31	72.567	29.305	28.844	1.00	66.29
ATOM	222	CD2	TYR	31	73.528	30.773	30.993	1.00	66.29
ATOM	223	CE2	TYR	31	73.120	31.424	29.832	1.00	66.29
ATOM	224	CZ	TYR	31	72.641	30.687	28.763	1.00	66.29
ATOM	225	OH	TYR	31	72.237	31.345	27.626	1.00	66.29
ATOM	226	C	TYR	31	75.562	28.609	34.276	1.00	51.94
ATOM	227	O	TYR	31	74.995	27.610	34.729	1.00	66.29
ATOM	228	N	MET	32	76.435	29.331	34.972	1.00	31.75
ATOM	229	CA	MET	32	76.788	29.013	36.351	1.00	31.75
ATOM	230	CB	MET	32	78.246	29.392	36.631	1.00	29.56
ATOM	231	CG	MET	32	78.807	28.822	37.925	1.00	29.56
ATOM	232	SD	MET	32	78.874	27.021	37.900	1.00	29.56
ATOM	233	CE	MET	32	80.515	26.716	38.506	1.00	29.56
ATOM	234	C	MET	32	75.857	29.820	37.246	1.00	31.75
ATOM	235	O	MET	32	75.576	30.984	36.960	1.00	29.56
ATOM	236	N	HIS	33	75.355	29.192	38.303	1.00	18.73
ATOM	237	CA	HIS	33	74.441	29.848	39.231	1.00	18.73
ATOM	238	CB	HIS	33	73.154	29.022	39.412	1.00	59.11
ATOM	239	CG	HIS	33	72.630	28.395	38.153	1.00	59.11
ATOM	240	CD2	HIS	33	73.216	27.574	37.249	1.00	59.11
ATOM	241	ND1	HIS	33	71.325	28.548	37.736	1.00	59.11
ATOM	242	CE1	HIS	33	71.130	27.850	36.631	1.00	59.11
ATOM	243	NE2	HIS	33	72.262	27.250	36.315	1.00	59.11
ATOM	244	C	HIS	33	75.136	29.943	40.584	1.00	18.73
ATOM	245	O	HIS	33	75.667	28.945	41.071	1.00	59.11

Table 13: Three dimensional coordinates of LC - CDR2 (ALA49 - SER55) from SB249417

ATOM	385	N	ALA	49	73.341	32.762	35.709	1.00	21.70
ATOM	386	CA	ALA	49	73.888	32.759	34.358	1.00	21.70
ATOM	387	CB	ALA	49	72.879	33.352	33.379	1.00	50.17
ATOM	388	C	ALA	49	75.206	33.523	34.298	1.00	21.70
ATOM	389	O	ALA	49	75.335	34.507	33.564	1.00	50.17
ATOM	390	N	THR	50	76.154	33.083	35.119	1.00	36.52
ATOM	391	CA	THR	50	77.494	33.655	35.211	1.00	36.52
ATOM	392	CB	THR	50	78.362	33.294	33.978	1.00	58.15
ATOM	393	OG1	THR	50	77.656	33.610	32.773	1.00	58.15
ATOM	394	CG2	THR	50	78.692	31.819	33.979	1.00	58.15
ATOM	395	C	THR	50	77.605	35.152	35.482	1.00	36.52
ATOM	396	O	THR	50	77.942	35.558	36.594	1.00	58.15
ATOM	397	N	SER	51	77.327	35.965	34.471	1.00	31.35
ATOM	398	CA	SER	51	77.441	37.413	34.592	1.00	31.35
ATOM	399	CB	SER	51	77.862	38.009	33.245	1.00	35.38
ATOM	400	OG	SER	51	79.126	37.511	32.836	1.00	35.38
ATOM	401	C	SER	51	76.228	38.169	35.120	1.00	31.35
ATOM	402	O	SER	51	76.352	39.325	35.528	1.00	35.38
ATOM	403	N	ASN	52	75.060	37.540	35.129	1.00	34.69
ATOM	404	CA	ASN	52	73.863	38.238	35.592	1.00	34.69
ATOM	405	CB	ASN	52	72.614	37.715	34.879	1.00	34.18
ATOM	406	CG	ASN	52	72.561	38.131	33.420	1.00	34.18
ATOM	407	OD1	ASN	52	72.529	39.322	33.102	1.00	34.18
ATOM	408	ND2	ASN	52	72.576	37.151	32.525	1.00	34.18
ATOM	411	C	ASN	52	73.653	38.278	37.098	1.00	34.69
ATOM	412	O	ASN	52	73.720	37.260	37.786	1.00	34.18
ATOM	413	N	LEU	53	73.386	39.480	37.593	1.00	28.58
ATOM	414	CA	LEU	53	73.156	39.733	39.008	1.00	28.58
ATOM	415	CB	LEU	53	73.805	41.074	39.380	1.00	36.89
ATOM	416	CG	LEU	53	73.657	41.716	40.761	1.00	36.89
ATOM	417	CD1	LEU	53	74.996	42.266	41.209	1.00	36.89
ATOM	418	CD2	LEU	53	72.624	42.829	40.711	1.00	36.89
ATOM	419	C	LEU	53	71.649	39.753	39.266	1.00	28.58
ATOM	420	O	LEU	53	70.876	40.229	38.432	1.00	36.89
ATOM	421	N	ALA	54	71.233	39.208	40.406	1.00	17.93
ATOM	422	CA	ALA	54	69.817	39.157	40.763	1.00	17.93
ATOM	423	CB	ALA	54	69.579	38.092	41.823	1.00	27.99
ATOM	424	C	ALA	54	69.307	40.507	41.248	1.00	17.93
ATOM	425	O	ALA	54	70.083	41.433	41.459	1.00	27.99
ATOM	426	N	SER	55	67.996	40.617	41.417	1.00	46.64
ATOM	427	CA	SER	55	67.390	41.857	41.881	1.00	46.64
ATOM	428	CB	SER	55	65.914	41.917	41.473	1.00	60.10
ATOM	429	OG	SER	55	65.769	41.953	40.062	1.00	60.10
ATOM	430	C	SER	55	67.513	41.947	43.396	1.00	46.64
ATOM	431	O	SER	55	67.249	40.973	44.104	1.00	60.10

Table 14: Three dimensional coordinates of LC - CDR3 (GLN88 - THR96) from SB249417

ATOM	677	N	GLN	88	76.228	26.138	40.949	1.00	23.98
ATOM	678	CA	GLN	88	75.808	24.954	40.213	1.00	23.98
ATOM	679	CB	GLN	88	74.400	24.510	40.616	1.00	33.56
ATOM	680	CG	GLN	88	73.285	25.370	40.066	1.00	33.56
ATOM	681	CD	GLN	88	71.932	24.738	40.259	1.00	33.56
ATOM	682	OE1	GLN	88	71.415	24.691	41.369	1.00	33.56
ATOM	683	NE2	GLN	88	71.346	24.251	39.179	1.00	33.56
ATOM	686	C	GLN	88	75.850	25.282	38.730	1.00	23.98
ATOM	687	O	GLN	88	75.909	26.452	38.349	1.00	33.56
ATOM	688	N	GLN	89	75.775	24.254	37.897	1.00	53.56
ATOM	689	CA	GLN	89	75.833	24.439	36.456	1.00	53.56
ATOM	690	CB	GLN	89	77.082	23.752	35.888	1.00	50.20
ATOM	691	CG	GLN	89	77.610	22.557	36.694	1.00	50.20
ATOM	692	CD	GLN	89	76.615	21.414	36.823	1.00	50.20
ATOM	693	OE1	GLN	89	75.598	21.532	37.510	1.00	50.20
ATOM	694	NE2	GLN	89	76.923	20.289	36.194	1.00	50.20
ATOM	697	C	GLN	89	74.596	23.944	35.728	1.00	53.56
ATOM	698	O	GLN	89	73.772	23.224	36.298	1.00	50.20
ATOM	699	N	TRP	90	74.447	24.383	34.481	1.00	42.71
ATOM	700	CA	TRP	90	73.331	23.967	33.641	1.00	42.71
ATOM	701	CB	TRP	90	73.336	24.762	32.327	1.00	107.30
ATOM	702	CG	TRP	90	72.630	24.093	31.185	1.00	107.30
ATOM	703	CD2	TRP	90	73.219	23.652	29.955	1.00	107.30
ATOM	704	CE2	TRP	90	72.197	23.037	29.200	1.00	107.30

ATOM	705	CE3	TRP	90	74.513	23.715	29.418	1.00107.30
ATOM	706	CD1	TRP	90	71.313	23.748	31.124	1.00107.30
ATOM	707	NE1	TRP	90	71.044	23.111	29.935	1.00107.30
ATOM	708	CZ2	TRP	90	72.427	22.485	27.935	1.00107.30
ATOM	709	CZ3	TRP	90	74.742	23.165	28.157	1.00107.30
ATOM	710	CH2	TRP	90	73.702	22.559	27.432	1.00107.30
ATOM	711	C	TRP	90	73.497	22.473	33.371	1.00 42.71
ATOM	712	O	TRP	90	72.522	21.720	33.366	1.00107.30
ATOM	713	N	SER	91	74.746	22.068	33.154	1.00 53.84
ATOM	714	CA	SER	91	75.130	20.683	32.897	1.00 53.84
ATOM	715	CB	SER	91	74.815	19.789	34.106	1.00 38.65
ATOM	716	OG	SER	91	73.457	19.379	34.150	1.00 38.65
ATOM	717	C	SER	91	74.545	20.057	31.639	1.00 53.84
ATOM	718	O	SER	91	73.464	20.425	31.184	1.00 38.65
ATOM	719	N	ILE	92	75.313	19.148	31.051	1.00 51.50
ATOM	720	CA	ILE	92	74.874	18.421	29.867	1.00 51.50
ATOM	721	CB	ILE	92	76.070	17.967	28.991	1.00 66.93
ATOM	722	CG2	ILE	92	75.598	17.678	27.570	1.00 66.93
ATOM	723	CG1	ILE	92	77.154	19.047	28.948	1.00 66.93
ATOM	724	CD1	ILE	92	78.444	18.594	28.271	1.00 66.93
ATOM	725	C	ILE	92	74.211	17.171	30.446	1.00 51.50
ATOM	726	O	ILE	92	73.268	16.621	29.881	1.00 66.93
ATOM	727	N	ASN	93	74.714	16.755	31.605	1.00 60.16
ATOM	728	CA	ASN	93	74.232	15.580	32.319	1.00 60.16
ATOM	729	CB	ASN	93	75.290	14.473	32.228	1.00 59.88
ATOM	730	CG	ASN	93	74.696	13.083	32.312	1.00 59.88
ATOM	731	OD1	ASN	93	74.187	12.673	33.354	1.00 59.88
ATOM	732	ND2	ASN	93	74.769	12.345	31.213	1.00 59.88
ATOM	735	C	ASN	93	74.046	16.023	33.775	1.00 60.16
ATOM	736	O	ASN	93	74.952	16.620	34.363	1.00 59.88
ATOM	737	N	PRO	94	72.883	15.709	34.377	1.00 45.30
ATOM	738	CD	PRO	94	72.057	14.607	33.849	1.00 61.85
ATOM	739	CA	PRO	94	72.443	16.011	35.740	1.00 45.30
ATOM	740	CB	PRO	94	72.227	14.621	36.314	1.00 61.85
ATOM	741	CG	PRO	94	71.516	13.930	35.137	1.00 61.85
ATOM	742	C	PRO	94	73.280	16.922	36.644	1.00 45.30
ATOM	743	O	PRO	94	74.461	16.670	36.913	1.00 61.85
ATOM	744	N	ARG	95	72.607	17.959	37.141	1.00 55.22
ATOM	745	CA	ARG	95	73.181	18.975	38.024	1.00 55.22
ATOM	746	CB	ARG	95	72.097	19.992	38.393	1.00 42.76
ATOM	747	CG	ARG	95	71.364	20.575	37.194	1.00 42.76
ATOM	748	CD	ARG	95	70.022	21.178	37.591	1.00 42.76
ATOM	749	NE	ARG	95	68.909	20.524	36.902	1.00 42.76
ATOM	750	CZ	ARG	95	67.634	20.899	36.995	1.00 42.76
ATOM	751	NH1	ARG	95	67.286	21.931	37.752	1.00 42.76
ATOM	754	NH2	ARG	95	66.701	20.246	36.315	1.00 42.76
ATOM	757	C	ARG	95	73.753	18.352	39.294	1.00 55.22
ATOM	758	O	ARG	95	73.351	17.255	39.684	1.00 42.76
ATOM	759	N	THR	96	74.657	19.066	39.963	1.00 47.74
ATOM	760	CA	THR	96	75.270	18.543	41.183	1.00 47.74
ATOM	761	CB	THR	96	76.630	17.877	40.875	1.00 32.33
ATOM	762	OG1	THR	96	77.370	18.701	39.967	1.00 32.33
ATOM	763	CG2	THR	96	76.433	16.494	40.264	1.00 32.33
ATOM	764	C	THR	96	75.456	19.495	42.370	1.00 47.74
ATOM	765	O	THR	96	75.379	19.052	43.515	1.00 32.33

References

Brünger A.T., (1990) *Acta Cryst.* A46:46-57.

Brünger A.T., (1991) *Acta Cryst.* A47:195-204.

Brünger A.T., *X-PLOR 3.0 Manual* (Yale University, 1992).

Huber R., (1985). In *Molecular Replacement.* Proc. of the Daresbury Study Weekend, Daresbury, February 1985, pp. 58-61. SERC Daresbury Laboratory, Daresbury, Warrington, England.

Monfardini C., Kieber-Emmons T., Voet D., Godillot A.P., Weiner D.B., Williams W.V., (1996) *J. Biol. Chem.* 271:2966-2971.

Otwinowski Z., "Oscillation Data Reduction," in *Proceedings of the CCP4 Study Weekend: "Data Collection and Processing," 29-30 January 1993*, comiled by L. Sawyer, N. Isaacs and S. Bailey (SERC Daresbury Laboratory, England), pp. 56-62.

Rossmann M.G. and Blow D.M., (1962). *Acta Cryst.* 15:24-31.

Rusinko, A., (1993) *Chem. Des. Auto. News* 8:44-47.

Zhao B., Helms L.R., DesJarlais R.L., Abdel-Meguid S.S. & Wetzel R., (1995) *Nature Struct. Biol.* 2:1131-1137.

The present invention may be embodied in other specific forms without departing from the spirit or essential attributes thereof, and, accordingly, reference should be made to the appended claims, rather than to the foregoing specification, as indicating the scope of the invention.

CLAIMS

1. A BC2 Fab fragment crystal.

2. A Fab fragment crystal containing BC2 complementarity determining regions (CDRs).

3. The crystal of claim 2 wherein the CDRs are characterized by the coordinates of Tables 3-8.

4. A SB249417 Fab fragment crystal.

5. The crystal of claim 4 wherein the CDRs are characterized by the coordinates of Tables 9-14.

6. A method for identifying a peptidomimetic having Factor IX binding activity comprising:

a. searching a small molecule structural database with CDR structural parameters derived from the crystal of claim 1, 2 or 4;

b. selecting a molecular structure from the database which mimics the CDR structural parameters;

c. synthesizing the selected molecular structure; and

d. screening the synthesized molecule for Factor IX binding activity.

7. The method of claim 6 wherein the synthesized molecule is further screened for antithrombotic activity.

8. The method of claim 7 wherein the synthesized molecule is further screened for self-limiting, neutralizing activity.

9. The method of claim 6 wherein the selected molecular structure mimics the parameters of CDR residues HC-Asn35, HC-Trp50, and LC-Arg95.

10. A computer-readable medium having BC2 CDR structural information stored thereon.

11. A computer-readable medium having SB249417 CDR structural information stored thereon.

Figure 1: BC2 HC – CDR1

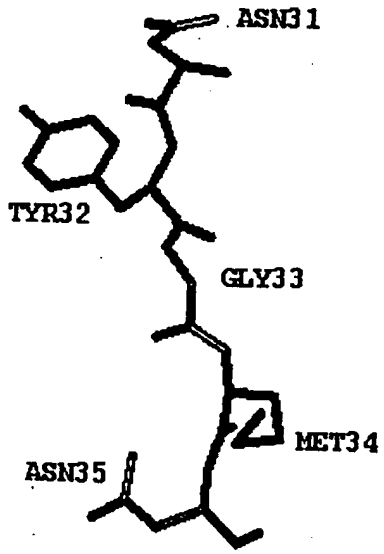


Figure 2: BC2 HC – CDR2

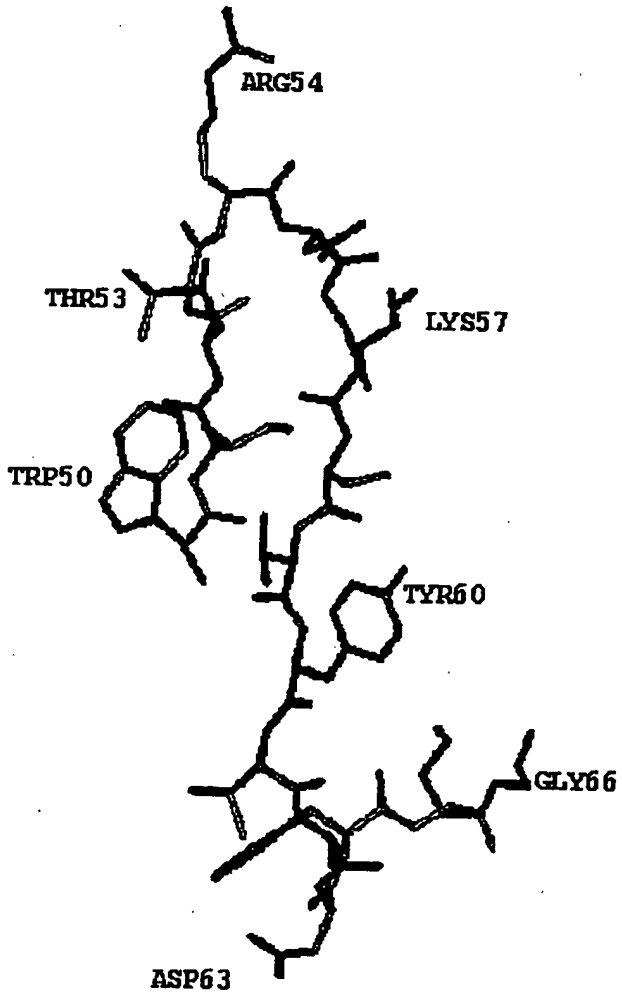


Figure 3: BC2 HC - CDR3

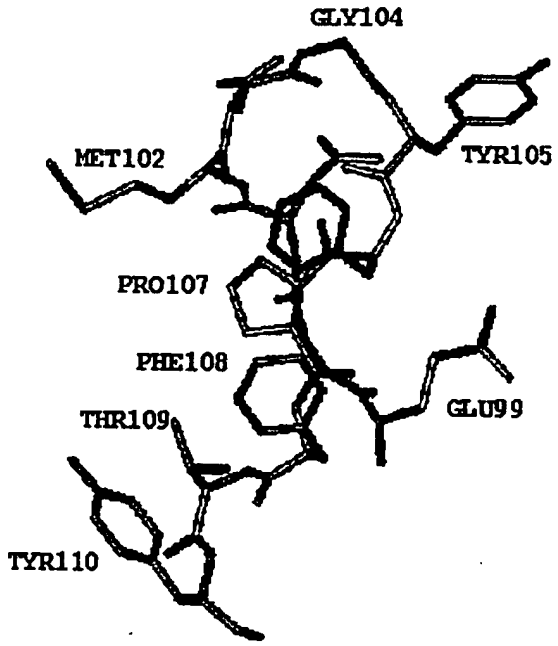


Figure 4: BC2 LC - CDR1

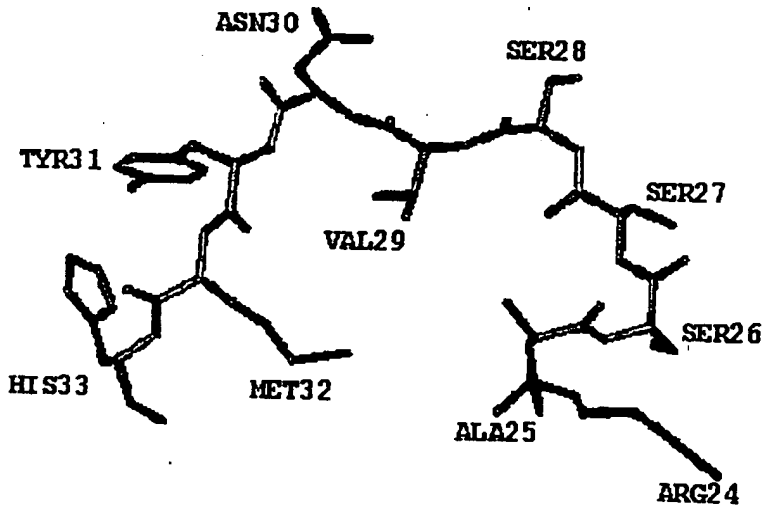


Figure 5: BC2 LC - CDR2

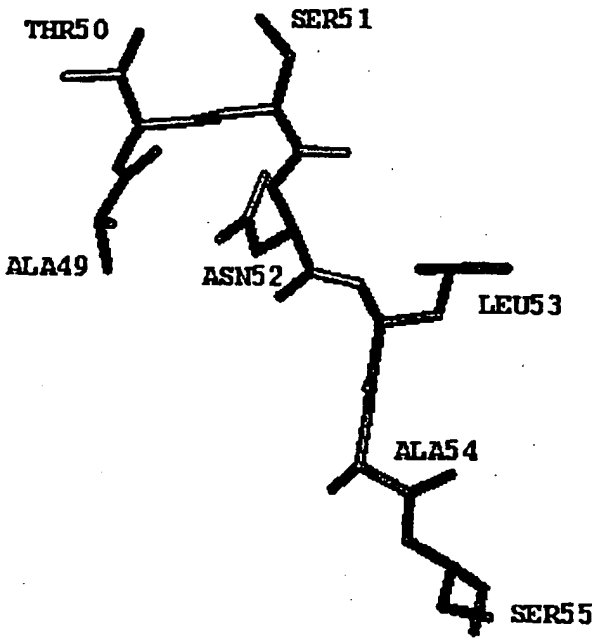


Figure 6: BC2 LC – CDR3

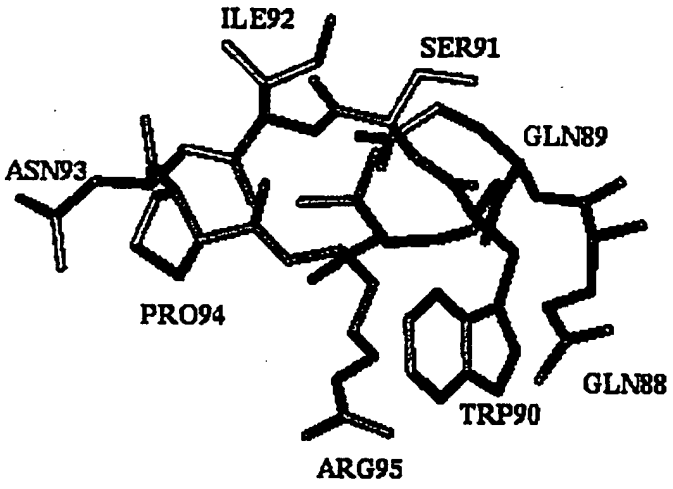


Figure 7: SB24917
HC – CDR1

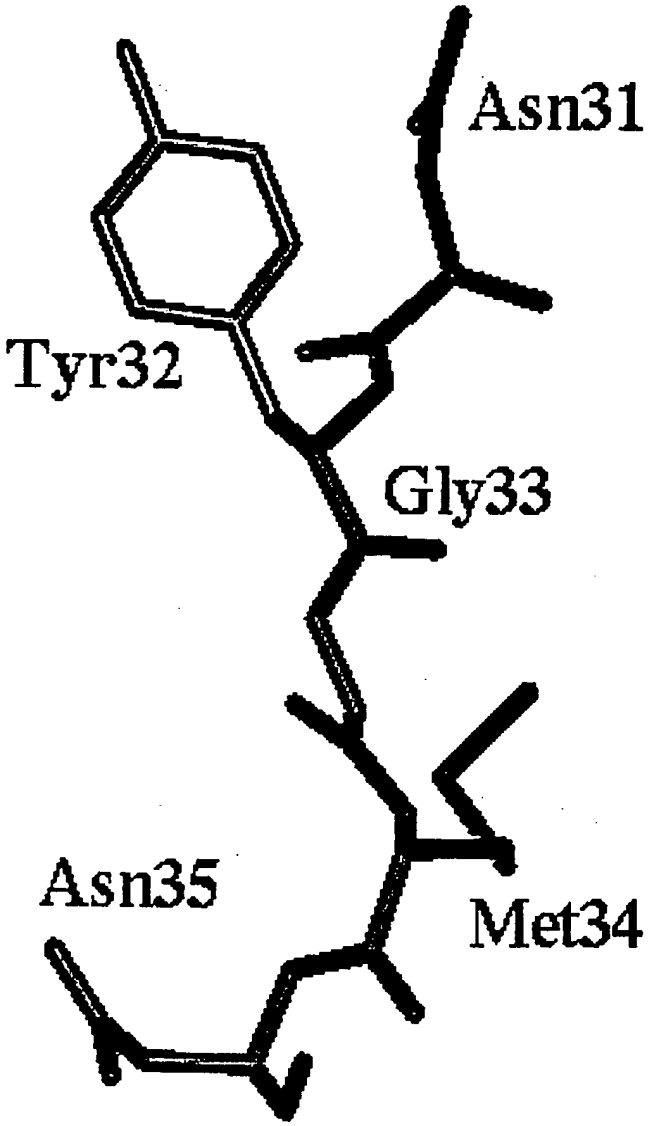


Figure 8: SB24917 HC - CDR2

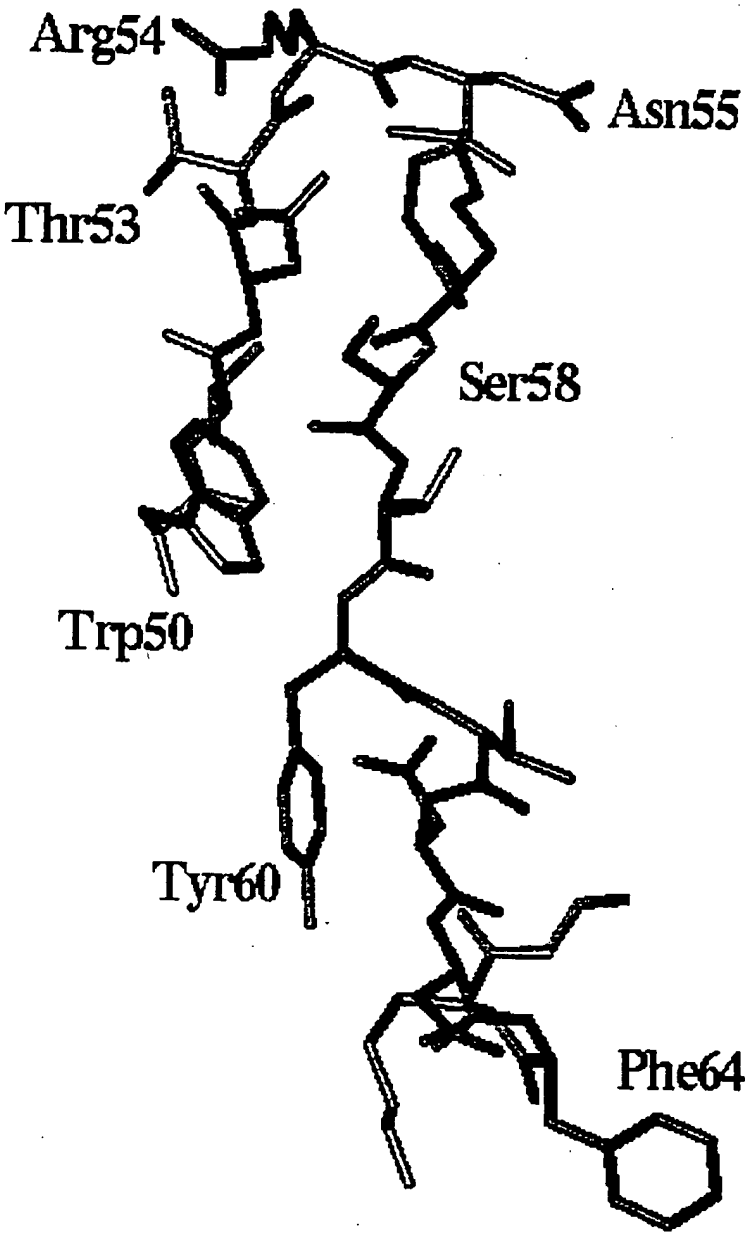


Figure 9: SB24917 HC CDR3

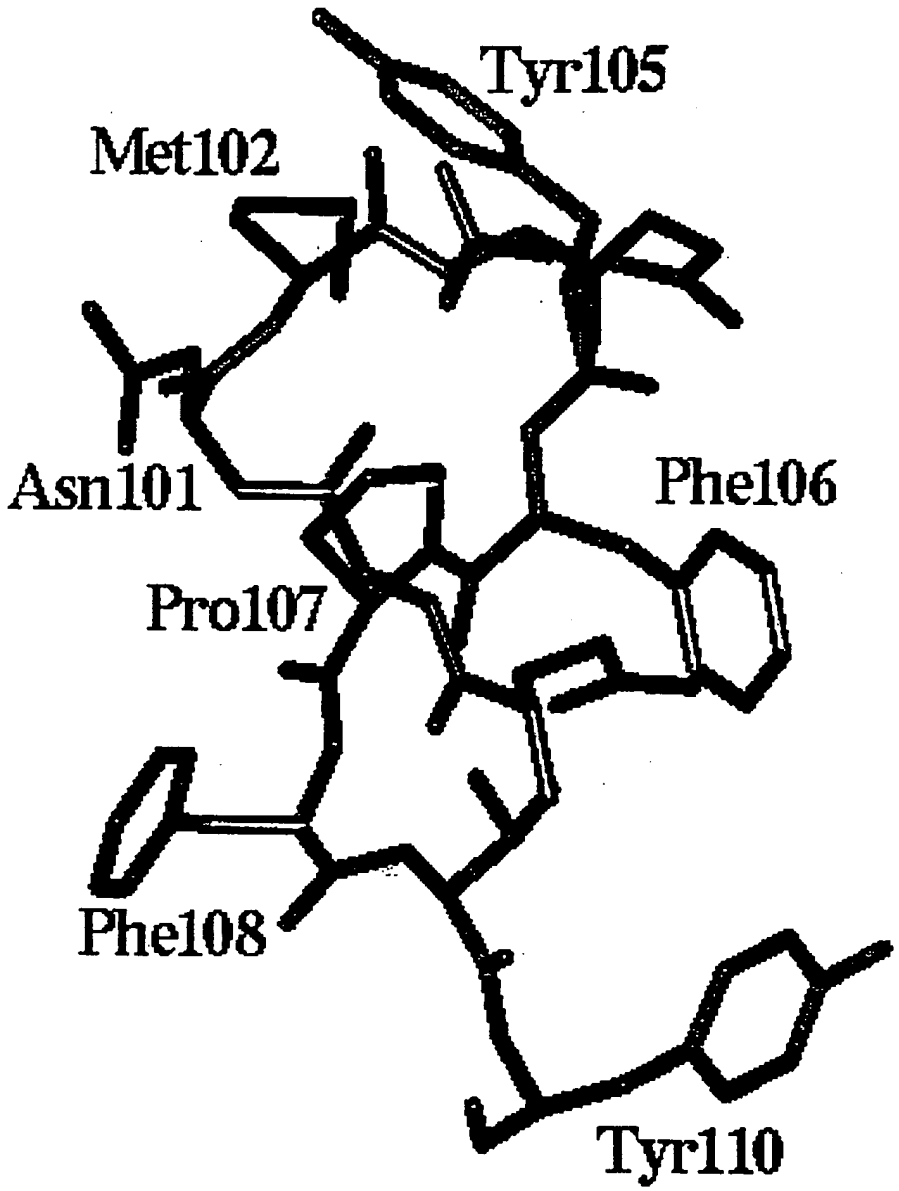


Figure 10: SB24917-L1 - CDR1

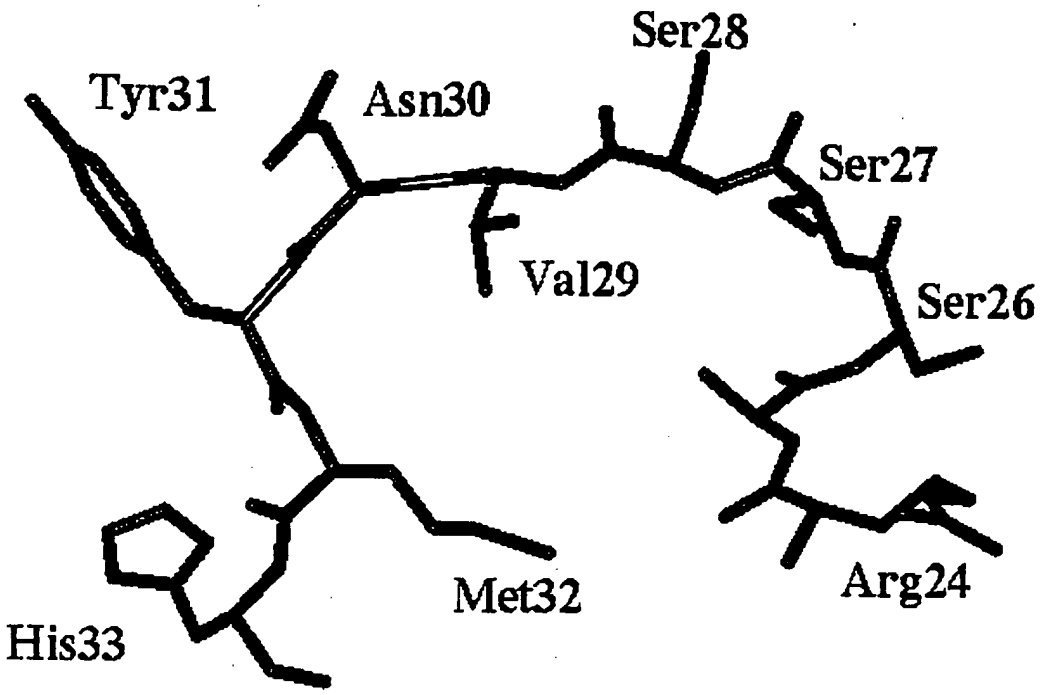


Figure 11: SB24917 LC- CDR2

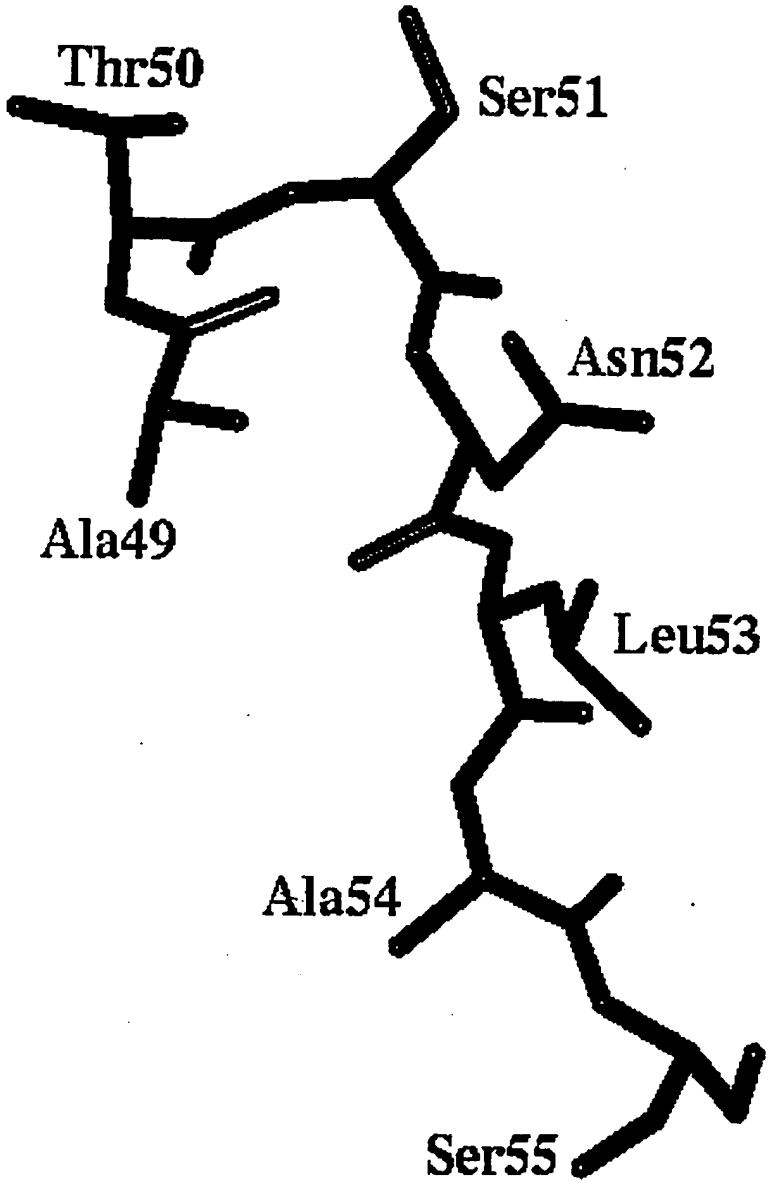
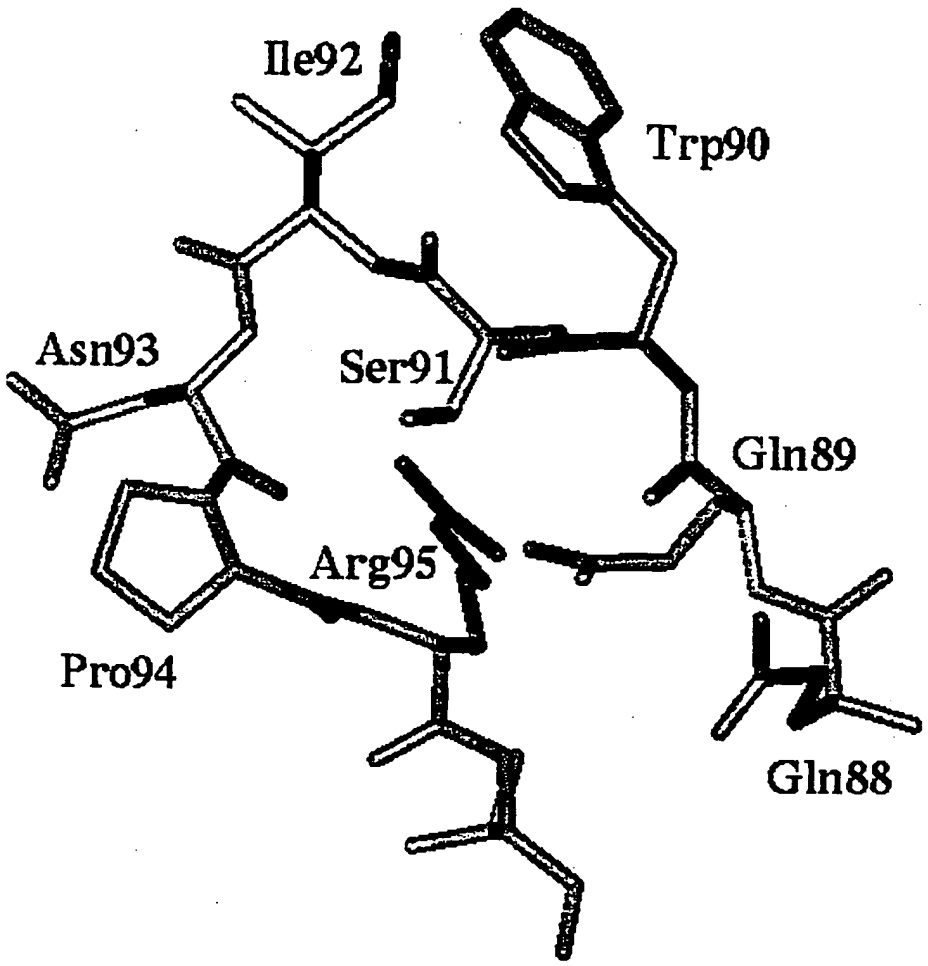


Figure 12: SB24917 .C – CDR3



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/13806

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C07K 16/00
US CL : 530/388.25

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/388.25; 530/388.22; 435/214; 514/18; 435/5; 530/381; 435/472; 530/381; 424/145.1; 514/56; 514/12; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Please See Extra Sheet.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE EXPRESS, APS, WEST

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MURRAY, C.W. PRO_SELECT: Combining structure-based drug design and combinatorial chemistry for rapid lead discovery.1. Technology. Journal of Computer-Aided Molecular Design. November 1997, Vol. 11, No. 2, pages 193-207 especially 194-197 and 204-206.	2-3, 5-7 and 9
Y	BOHM, HANS-JOACHIM. The Computer Program: LUDI: A New Method For The de novo Design of Enzyme Inhibitors. Journal of Computer-Aided Molecular Design. August 1991, Vol 78. No. 143, page 61-78, especially 62.	1 and 6
Y	MARTIN, Y.C. 3D Database Searching in Drug Design. Journal of Medicinal Chemistry. June 1992, Vol 35, No. 12, pages 2139-2154, especially pages 2149-2151.	6-8

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search	Date of mailing of the international search report
05 NOVEMBER 1998	17 DEC 1998
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer JA-NA HINES Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/13806

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y,P	US 5,739,277 A (PRESTA et al) 14 April 1998, col. 5, lines 19-21, col. 6 lines 37-65, col. 8 lines 25-47.	1 and 2
X,P	WO 97/26010 A1 (SMITHKLINE BEECHAM CORPORATION) 24 July 1997, page 1-20	1-8

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/13806

B. FIELDS SEARCHED
Documentation other than minimum documentation that are included in the fields searched:

Journal of Medicinal Chemistry, Journal of Computer-Aided Molecular Design, Nucleic Acids Research, Journal of Biological Chemistry, Blood Coagulation and Fibrinolysis, Nature Structual Biology